(19) Europäisches Patentamt
European Patent Office
Office européen des brevets

(11) Publication number: **0 408 403 B1**

(12) EUROPEAN PATENT SPECIFICATION

(45) Date of publication of patent specification: **03.08.94 Bulletin 94/31**

(51) Int. Cl.[5]: **C12N 15/32**, A01N 63/00

(21) Application number: **90401427.1**

(22) Date of filing: **29.05.90**

(54) Prevention of resistance development against Bacillus thuringiensis insecticidal crystal protein.

(30) Priority: **31.05.89 EP 89401499**

(43) Date of publication of application: **16.01.91 Bulletin 91/03**

(45) Publication of the grant of the patent: **03.08.94 Bulletin 94/31**

(84) Designated Contracting States: **AT BE CH DE DK ES FR GB GR IT LI LU NL SE**

(56) References cited:
EP-A- 0 192 319
EP-A- 0 193 259
EP-A- 0 221 024
EP-A- 0 228 838
WO-A-88/08880
PATENT ABSTRACTS OF JAPAN, vol. 12, no. 391 (C-537)(3238), 18 Oct. 1988; & JP-A-63 137 684
PATENT ABSTRACTS OF JAPAN, vol. 13, no. 326 (C-620), 24 July 1989; & JP-A-01 104 177

(56) References cited:
CHEMICAL ABSTRACTS, vol. 112, no. 21, 21 May 1990, p. 262, abstract no. 193742f, Columbus, Ohio, US; G. HONEE et al, "A translation fusion product of two different insecticidal crystal protein genes of Bacillus thuringiensis exhibits an enlarged insecticidal spectrum"
Hofmann, C. et al. Eur. J. Biochem. Vol. 173, pp. 85-91 (1988)
Hofmann, C. et al. Proc. Natl. Acad. Sci. USA Vol. 85, pp 7844-7848 (November 1988)

(73) Proprietor: **PLANT GENETIC SYSTEMS, N.V.**
Kolonel Bourgstraat 106
Bus 1
B-1040 Brussel (BE)

(72) Inventor: **Van Mellaert, Herman**
Wilselsesteenweg 19
B-3200 Leuven (BE)
Inventor: **Botterman, Johan**
Het Wijngaardeke 5
B-9721 Zevergem - De Pinte (BE)
Inventor: **Van Rie, Jeroen**
Gravin Johannalaan 10
B-9900 Eeklo (BE)
Inventor: **Joos, Henk**
Oostmolen Zuid 5
B-9880 Aalter (BE)

(74) Representative: **Gutmann, Ernest et al**
Ernest Gutmann - Yves Plasseraud S.A.
3, rue Chauveau-Lagarde
F-75008 Paris (FR)

EP 0 408 403 B1

Description

This invention relates to plant cells and plants, the genomes of which are transformed to contain at least two genes, each coding for a different non-competitively binding Bacillus thuringiensis ("B. thuringiensis" or "Bt") insecticidal crystal protein ("ICP") for a specific target insect species, preferably belonging to the order of Lepidoptera or Coleoptera. Such transformed plants have advantages over plants transformed with a single B. thuringiensis ICP gene, especially with respect to the prevention of resistance development in the target insect species against the at least two B. thuringiensis ICPs, expressed in such plants.

This invention also relates to a process for the production of such transgenic plants, taking into account the competitive and non-competitive binding properties of the at least two B. thuringiensis ICPs in the target insect species' midgut. Simultaneous expression in plants of the at least two genes, each coding for a different non-competitively binding B. thuringiensis ICP in plants, is particularly useful to prevent or delay resistance development of insects against the at least two B. thuringiensis ICPs expressed in the plants.

This invention further relates to a process for the construction of novel plant expression vectors and to the novel plant expression vectors themselves, which contain the at least two B. thuringiensis ICP genes encoding the at least two non-competitively binding B. thuringiensis ICPs. Such vectors allow integration and coordinate expression of the at least two B. thuringiensis ICP genes in plants.

BACKGROUND OF THE INVENTION

Since the development and the widespread use of chemical insecticides, the occurrence of resistant insect strains has been an important problem. Development of insecticide resistance is a phenomenon dependent on biochemical, physiological, genetic and ecological mechanisms. Currently, insect resistance has been reported against all major classes of chemical insecticides including chlorinated hydrocarbons, organophosphates, carbamates, and pyrethroid compounds (Brattsten et al., 1986).

In contrast to the rapid development of insect resistance to synthetic insecticides, development of insect resistance to bacterial insecticides such as B. thuringiensis sprays has evolved slowly despite many years of use (Brattsten et al., 1986). The spore forming gram-positive bacterium B. thuringiensis produces a parasporal crystal which is composed of crystal proteins (ICPs) having insecticidal activity. Important factors decreasing the probability of emergence of resistant insect strains in the field against B. thuringiensis sprays are: firstly the short half-life of B. thuringiensis sprays after foliar application; secondly the fact that commercial B. thuringiensis preparations often consist of a mixture of several insecticidal factors including spores, ICPs and eventually beta-exotoxins (Shields, 1987); and thirdly the transitory nature of plant-pest interactions. Many successful field trials have shown that commercial preparations of a B. thuringiensis containing its spore-crystal complex, effectively control lepidopterous pests in agriculture and forestry (Krieg and Langenbruch, 1981). B. thuringiensis is at present the most widely used pathogen for microbial control of insect pests.

Various laboratory studies, in which selection against B. thuringiensis was applied over several generations of insects, have confirmed that resistance against B. thuringiensis is seldom obtained. However, it should be emphasized that the laboratory conditions represented rather low selection pressure conditions.

For example, Goldman et al. (1986) have applied selection with B. thuringiensis israelensis toxin over 14 generations of Aedes aegypti and found only a marginal decrease in sensitivity. The lack of any observable trend toward decreasing susceptibility in the selected strains may be a reflection of the low selection pressure (LC_{50}) carried out over a limited number of generations. However, it should be pointed out that Georghiou et al. (In : Insecticide Resistance in Mosquitoes : Research on new chemicals and techniques for management. In "Mosquito Control Research, Annual Report 1983, University of California.") with Culex quinquefasciatus obtained an 11-fold increase in resistance to B. thuringiensis israelensis after 32 generations at LC_{95} selection presssure.

McGaughey (1985) reported that the grain storage pest Plodia interpunctella developed resistance to the spore-crystal complex of B. thuringiensis; after 15 generations of selection with the Indian meal moth, Plodia interpunctella, using a commercial B. thuringiensis HD-1 preparation ("Dipel", Abbott Laboratories, North Chicago, Illinois 60064, USA), a 100-fold decrease in B. thuringiensis sensitivity was reported. Each of the colonies was cultured for several generations on a diet treated with a constant B. thuringiensis dosage which was expected to produce 70-90% larval mortality. Under these high selection press sure conditions, insect resistance to B. thuringiensis increased rapidly. More recently, development of resistance against B. thuringiensis is also reported for the almond moth, Cadra cautella (McGaughey and Beeman, 1988). Resistance was stable when selection was discontinued and was inherited as a recessive trait (McGaughey and Beeman, 1988). The mechanism of insect resistance to B. thuringiensis toxins of Plodia interpunctella and Cadra cautella has not been elucidated.

The main cause of B. thuringiensis resistance development in both reported cases involving grain storage was the environmental conditions prevailing during the grain storage. Under the conditions in both cases, the environment was relatively stable, so B. thuringiensis degradation was slow and permitted successive generations of the pest to breed in the continuous presence of the microbial insecticide. The speed at which Plodia developed resistance to B. thuringiensis in one study suggests that it could do so within one single storage season in the bins of treated grain.

Although insect resistance development against B. thuringiensis has mostly been observed in laboratory and pilot scale studies, very recent indications of B. thuringiensis resistance development in Plutella xylostella populations in the (cabbage) field have been reported (Kirsch and Schmutterer, 1988). A number of factors have led to a continuous exposure of P. xylostella to B. thuringiensis in a relatively small geographic area. This and the short generation cycle of P. xylostella have seemingly led to an enormous selection pressure resulting in decreased susceptibility and increased resistance to B. thuringiensis.

A procedure for expressing a B. thuringiensis ICP gene in plants in order to render the plants insect-resistant (European patent publication ("EP") 0193259 Vaeck et al., 1987; Barton et al., 1987; Fischhoff et al., 1987) provides an entirely new approach to insect control in agriculture which is at the same time safe, environmentally attractive and cost-effective. An important determinant for the success of this approach will be whether insects will be able to develop resistance to B. thuringiensis ICPs expressed in transgenic plants (Vaeck et al., 1987; Barton et al., 1987; Fischhoff et al., 1987). In contrast with a foliar application, after which B. thuringiensis ICPs are rapidly degraded, the transgenic plants will exert a continuous selection pressure. It is clear from laboratory selection experiments that a continuous selection pressure has led to adaptation to B. thuringiensis and its components in several insect species. In this regard, it should be pointed out that the conditions in the laboratory which resulted in the development of insect-resistance to B. thuringiensis are very similar to the situation with transgenic plants which produce B. thuringiensis ICPs and provide a continuous selection pressure on insect populations feeding on the plants. Mathematical models of selection pressure predict that, if engineered insect-resistant plants become a permanent part of their environment, resistance development in insects will emerge rapidly (Gould, 1988). Thus, the chances for the development of insect resistance to B. thuringiensis in transgenic plants may be considerably increased as compared to the field application of B. thuringiensis sprays. A Heliothis virescens strain has been reported that is 20 times more resistant to B. thuringiensis HD-1 ICP produced by transgenic Pseudomonas fluorescens and 6 times more resistant to the pure ICP (Stone et al., 1989). Furthermore, the monetary and human costs of resistance are difficult to assess, but loss of pesticide effectiveness invariably entails increased application frequencies and dosages and, finally, more expensive replacement compounds as new pesticides become more difficult to discover and develop.

Therefore, it would be desirable to develop means for delaying or even preventing the evolution of resistance to B. thuringiensis.

B. thuringiensis strains, active against Lepidoptera (Dulmage et al., 1981), Diptera (Goldberg and Margalit, 1977) and Coleoptera (Krieg et al., 1983), have been described. It has become clear that there is a substantial heterogeneity among ICPs from different strains active against Lepidoptera, as well as among ICPs from strains active against Coleoptera (Hofte and Whiteley, 1989). An overview of the different B. thuringiensis ICP genes, that have been characterized, is given in Table 2 (which follows the Examples herein).

Most of the anti-Lepidopteran B. thuringiensis (e.g., Bt3, Bt2, Bt73, Bt14, Bt15, Bt4, Bt18) ICP genes encode 130 to 140 kDa protoxins which dissolve in the alkaline environment of an insect's midgut and are proteolytically activated into an active toxin of 60-65 kDa. These ICPs are related and can be recognized as members of the same family based on sequence homologies. The sequence divergence however is substantial, and the insecticidal spectrum, among the order Lepidoptera, may be substantially different (Höfte et al., 1988).

The P2 toxin gene and the cry B2 gene are different from the above-mentioned genes in that they do not encode high molecular weight protoxins but rather toxins of around 70 kDa (Donovan et al., 1988 and Widner and Whiteley, 1989, respectively).

It has recently become clear that heterogeneity exists also in the anti-Coleopteran toxin gene family. Whereas several previously reported toxin gene sequences from different B. thuringiensis isolates with anti-Coleopteran activity were identical (EP 0149162 and 0202739), the sequences and structure of bt21 and bt22 are substantially divergent (European patent application ("EPA") 89400428.2).

While the insecticidal spectra of B. thuringiensis ICPs are different, the major pathway of their toxic action is believed to be common. All B. thuringiensis ICPs, for which the mechanism of action has been studied in any detail, interact with the midgut epithelium of sensitive species and cause lysis of the epithelial cells (Knowles and Ellar, 1986) due to the fact that the permeability characteristics of the brush border membrane and the osmotic balance over this membrane are perturbed. In the pathway of toxic action of B. thuringiensis ICPs, the binding of the toxin to receptor sites on the brush border membrane of these cells is an important

feature (Hofmann et al., 1988b). The toxin binding sites in the midgut can be regarded as an ICP-receptor since toxin is bound in a saturable way and with high affinity (Hofmann et al., 1988a).

Although this outline of the mode of action of B. thuringiensis ICPs is generally accepted, it remains a matter of discussion what the essential determinant(s) are for the differences in their insecticidal spectra. Haider et al. (1986) emphasize the importance of specific proteases in the insect midgut. Hofmann et al. (1988b) indicate that receptor binding is a prerequisite for toxic activity and describe that Pieris brassicae has two distinct receptor populations for two toxins. Other authors have suggested that differences in the environment of the midgut (e.g., pH of the midgut) might be crucial.

SUMMARY OF THE INVENTION

In accordance with this invention, a plant is provided having, stably integrated into its genome, at least two B. thuringiensis ICP genes encoding at least two non-competitively binding insecticidal B. thuringiensis ICPs, preferably the active toxins thereof, against a specific target insect, preferably against a Lepidoptera or Coleoptera. Such a plant is characterized by the simultaneous expression of the at least two non-competitively binding B. thuringiensis ICPs.

Also in accordance with this invention, at least two ICP genes, particularly two genes or parts thereof coding for two non-competitively binding anti-Lepidopteran or anti-Coleopteran B. thuringiensis ICPs, are cloned into a plant expression vector. Plant cells transformed with this vector are characterized by the simultaneous expression of the at least two B. thuringiensis ICP genes. The resulting transformed plant cell can be used to produce a transformed plant in which the plant cells: 1. contain the at least two B. thuringiensis ICP genes or parts thereof encoding at least two non-competitively binding anti-Lepidopteran or anti-Coleopteran B. thuringiensis ICPs as a stable insert into their genome; and 2. express the genes simultaneously, thereby conferring on the plant improved resistance to at least one target species of insect, so as to prevent or delay development of resistance to B. thuringiensis of the at least one target species of insect feeding on the transformed plant.

Further in accordance with this invention, plant expression vectors are provided which allow integration and simultaneous expression of at least two B. thuringiensis ICP genes in a plant cell and which comprise one or more chimeric genes, each containing in the same transcriptional unit: a promoter which functions in the plant cell to direct the synthesis of mRNA encoded by one of the ICP genes; one or more different ICP genes, each encoding a non-competitively binding B. thuringiensis ICP; preferably a marker gene; a 3' non-translated DNA sequence which functions in the plant cell for 3' end formation and the addition of polyadenylate nucleotides to the 3' end of the mRNA; and optionally a DNA sequence encoding a protease-sensitive protein part between any two ICP genes.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

As used herein, "B. thuringiensis ICP" (or "ICP") should be understood as an intact protein or a part thereof which has insecticidal activity and which can be produced in nature by B. thuringiensis. An ICP can be a protoxin, as well as an active toxin or another insecticidal truncated part of a protoxin which need not be crystalline and which need not be a naturally occurring protein. In this regard, an ICP can be a chimaeric toxin encoded by the combination of two variable regions of two different ICP genes as disclosed in EP 0228838.

As used herein, "protoxin" should be understood as the primary translation product of a full-length gene encoding an ICP.

As used herein, "toxin", "toxic core" or "active toxin" should all be understood as a part of a protoxin which can be obtained by protease (e.g., by trypsin) cleavage and has insecticidal activity.

As used herein, "gene" should be understood as a full-length DNA sequence encoding a protein (e.g., such as is found in nature), as well as a truncated fragment thereof encoding at least the active part (i.e., toxin) of the protein encoded by the full-length DNA sequence, preferably encoding just the active part of the protein encoded by the full-length DNA sequence. A gene can be naturally occurring or synthetic.

As used herein, "truncated B. thuringiensis gene" should be understood as a fragment of a full-length B. thuringiensis gene which still encodes at least the toxic part of the B. thuringiensis ICP, preferentially the toxin.

As used herein, "marker gene" should be understood as a gene encoding a selectable marker (e.g., encoding antibiotic resistance) or a screenable marker (e.g., encoding a gene product which allows the quantitative analysis of transgenic plants).

Two ICPs are said to be "competitively binding ICPs" for a target insect species when one ICP competes

for all ICP receptors of the other ICP, which receptors are present in the brush border membrane of the midgut of the target insect species.

Two ICPs are said to be "non-competitively binding ICPs" when, for at least one target insect species, the first ICP has at least one receptor for which the second ICP does not compete and the second ICP has at least one receptor for which the first ICP does not compete, which receptors are present in the brush border membrane of the midgut of the target insect species.

A "receptor" should be understood as a molecule, to which a ligand (here a B. thuringiensis ICP, preferably a toxin) can bind with high affinity (typically a dissociation constant (Kd) between 10^{-11} and 10^{-6}M) and saturability. A determination of whether two ICPs are competitively or non-competitively binding ICPs can be made by determining whether: 1. a first ICP competes for all of the receptors of a second ICP when all the binding sites of the second ICP with an affinity in the range of about 10^{-11} to 10^{-6}M can be saturated with the first ICP in concentrations of the first ICP of about 10^{-5}M or less (e.g., down to about 10^{-11}M); and 2. the second ICP competes for the all of the receptors of the first ICP when all the binding sites of the first ICP with an affinity in the range of about 10^{-11} to 10^{-6}M can be saturated with the second ICP in concentrations of the second ICP of about 10^{-5}M or less.

General Procedures

This section describes in broad terms general procedures for the evaluation and exploitation of at least two B. thuringiensis ICP genes for prevention of the development, in a target insect, of a resistance to the B. thuringiensis ICPs expressed in transgenic plants of this invention. A non-exhaustive list of consecutive steps in the general procedure follows, after which are described particular Examples that are based on this methodology and that illustrate this invention.

In accordance with this invention, specific B. thuringiensis ICPs can be isolated in a conventional manner from the respective strains such as are listed in Table 2 (which follows the Examples). The ICPs can be used to prepare monoclonal or polyclonal antibodies specific for these ICPs in a conventional manner (Höfte et al., 1988).

The ICP genes can each be isolated from their respective strains in a conventional manner. Preferably, the ICP genes are each identified by: digesting total DNA from their respective strains with suitable restriction enzyme(s); size fractionating the DNA fragments, so produced, into DNA fractions of 5 to 10 Kb; ligating such fractions to suitable cloning vectors (e.g., pEcoR251, deposited at the Deutsche Sammlung von Mikroorganismen und Zellculturen ("DSM"), Braunschweig, Federal Republic of Germany, under accession number no. 4711 on July 13, 1988); transforming E.coli with the cloning vectors; and screening the clones with a suitable DNA probe. The DNA probe can be constructed from a highly conserved region which is commonly present in different B. thuringiensis genes which encode crystal protoxins against Coleoptera or Lepidoptera, such as on the basis of an N-terminal amino acid sequence determined by gas-phase sequencing of the purified proteins (EPA 88402115.5).

Alternatively, the desired fragments, prepared from total DNA of the respective strains, can be ligated in suitable expression vectors (e.g., a pUC vector (Yanisch-Perron et al., 1985) with the insert under the control of the lac promoter) and transformed in E. coli, and the clones can then be screened by conventional colony immunoprobing methods (French et al., 1986) for expression of the toxins with monoclonal or polyclonal antibodies raised against the toxins produced by the strains.

The isolated B. thuringiensis ICP genes can then be sequenced in a conventional manner using well-known procedures (e.g., Maxam and Gilbert, 1980).

At present, several ICP genes have been cloned from different subspecies of B. thuringiensis (Table 2). The nucleotide sequences from several of these B. thuringiensis ICP genes have been reported. whereas several sequences are identical or nearly identical and represent the same gene or slight variants of the same gene, several sequences display substantial heterogeneity and show the existence of different B. thuringiensis ICP gene classes. Several lines of evidence suggest that all these genes specify a family of related insecticidal proteins. Analysis of the distribution of B. thuringiensis ICPs in different B. thuringiensis strains by determining the protein composition of their crystals, by immunodetection using polyclonal antisera or monoclonals against purified crystals, or by using gene-specific probes, shows that subspecies of B. thuringiensis might contain up to three related B. thuringiensis ICP genes belonging to different classes (Kronstad et al., 1983).

To express the isolated and characterized gene in a heterologous host for purification and characterization of the recombinant protein, the preferred organism is Escherichia coli. A number of expression vectors for enhanced expression of heterologous genes in E. coli have been described (e.g., Remaut et al., 1981). Usually the gene is cloned under control of a strong regulatable promoter, such as the lambda pL or pR promoters (e.g., Botterman and Zabeau, 1987), the lac promoter (e.g., Fuller, 1982) or the tac promoter (e.g., De Boer et

al., 1983), and provided with suitable translation initiation sites (e.g., Stanssens et al, 1985 and 1987). Gene cassettes of the B. thuringiensis ICP genes can be generated by site-directed mutagenesis, for example according to the procedure described by Stanssens et al. (1985 and 1987). This allows cassettes to be made comprising, for example, a truncated ICP gene fragment encoding the toxic core (i.e., toxin) of an ICP or a hybrid gene encoding the toxic core and a selectable marker according to the procedures described in EPA 88402241.9.

The cells of an E. coli culture, which has been induced to produce a recombinant ICP, are harvested. The method used to induce the cells to produce the recombinant ICP depends on the choice of the promoter. For example, the lac promoter (Fuller, 1982) is induced by isopropyl-B-D-thiogalacto-pyranoside ("IPTG"); the pL promoter is induced by temperature shock (Bernard et al., 1979). The recombinant ICP is usually deposited in the cells as insoluble inclusions (Hsuing and Becker, 1988). The cells are lysed to liberate the inclusions. The bulk of E. coli proteins is removed in subsequent washing steps. A semi-purified protoxin pellet is obtained, from which the protoxin can be dissolved in alkaline buffer (e.g., Na_2CO_3, pH 10). The procedure for the ICP Bt2, which is also applicable to other recombinant toxins, has been described by Höfte et al., 1986.

In accordance with this invention, the binding of various ICPs to ICP receptors on the brush border membrane of the columnar midgut epithelial cells of various insect species has been investigated. The brush border membrane is the primary target of each ICP, and membrane vesicles, preferentially derived from the brush border membrane, can be obtained according to Wolfersberger et al., 1987.

The binding to ICP receptors of one or more ICPs (e.g., ICP A, ICP B, etc.) can be characterized by the following steps (Hofmann et al, 1988b):

1. ICP A is labelled with a suitable marker (usually a radioisotope such as ^{125}I).
2. Brush border membranes are incubated with a small amount (preferably less than 10^{-10} M) of labelled ICP A together with different concentrations of non-labelled ICP A (preferably from less than 10^{-11} to 10^{-5} M).
3. For all concentrations tested the amount of labelled ICP A bound to the brush border membranes is measured.
4. Mathematical analysis of these data allows one to calculate various characteristics of the ICP receptor such as the magnitude of the population of binding sites (Scatchard, 1949).
5. Competition by other toxins (e.g. ICP B) is preferably studied by incubating the same amount of labelled ICP A with brush border membranes in combination with different amounts of ICP B (preferentially from 10^{-11} to 10^{-6} M; and subsequently, steps 3 and 4 are repeated.

By this procedure, it has been found, for example, that Bt3 toxin, Bt2 toxin and Bt73 toxin are competitively binding anti-Lepidopteran ICPs for Manduca sexta and Heliothis virescens (See example 6 which follows). Various other combinations of toxins have been found to be non-competitively binding anti-Lepidopteran or anti-Coleopteran toxins (example 6).

Although the concept of competitivity versus non-competitivity of ICP binding does not have any practical importance by itself, the observation of the non-competitivity of two B. thuringiensis ICPs, active against the same target insect, can be put to very significant practical use. This is because a combination of two non-competitively binding B. thuringiensis ICPs can be used to prevent development, by a target insect, of resistance against such B. thuringienis ICPs.

A selection experiment with M. sexta, using Bt2 toxin, Bt18 toxin, and a mixture of Bt2 and Bt18 toxins, has shown that Bt2 and Bt18 are two non-competitively binding anti-Lepidopteran toxins. After 20 generations of selection, a very pronounced reduction in ICP sensitivity was observed in the selection experiments with Bt2 or Bt18 alone (>100 times). The reduction in sensitivity in the selection experiment with a Bt2-Bt18 mixture was only marginal (3 times). This demonstrates the unexpected practical advantage of a simultaneous use of two non-competitively binding ICPs in a situation which models the high selection pressure which will exist with the use of transgenic plants transformed with ICP genes. In this regard, the two resistant strains showed a specific loss in receptor sites for either the Bt2 or Bt18 toxin. In each case, receptor sites for the toxin, which was not used for selection, were not affected or their concentration even increased. Thus, the Bt2 selected strain retained its Bt18 receptors, and the Bt18 selected strain developed an increased number of Bt2 receptors. Indeed, the Bt18 selected strain showed an increased sensitivity for Bt2 along with its increased Bt2 receptor concentration. No significant changes in receptor sites were found in the strain selected against the combined toxins. These findings are described in detail in Example 7 which follows.

A similar mechanism of resistance to Bt has been observed with respect to a strain of diamondback moth, Plutella xylostella. This strain had developed resistance in the field to Dipel which is a commercial formulation of the Bt HD-1 strain. Crystals of Dipel comprise a mixture of several BtICPs, similar to the Bt2, Bt3 and Bt73 proteins which are competitively-binding ICPs. As shown by both insect bioassays and competitive binding studies using Bt2 and Bt15, the Dipel-resistant diamondback moth strain is resistant to Bt2 protoxin and toxin

but maintains full sensitivity to Bt15 protoxin and toxin. This finding is relevant to other combinations of non-competitively binding anti-Lepidopteran or Coleopteran ICPs which are expected to have the same beneficial effect against their common target insects.

Hence, a combination of non-competitively binding ICPs, when directly expressed in a transgenic plant, offers the substantial advantage of reducing the chances of development of insect resistance against the ICPs expressed in the plant. There may be additional benefits because the combined spectrum of two toxins may be broader than the spectrum of a single ICP expressed in a plant (See Examples 8, 9 and 10 which follow).

If, among two competitively binding ICPs, one has a larger binding site population than the other against a given target insect, it will be most advantageous to use the one with the larger population of binding sites to control the target pest in combination with the most suitable non-competitively binding B. thuringiensis ICP. For example, as seen from Example 6, it is preferred to use Bt73 against Hellothis virescens, rather than Bt2 or Bt3, and it is preferred to use Bt3 against Manduca sexta rather than Bt2 or Bt73. The selected gene can then be combined with the best suitable non-competitively binding ICP.

Previously, plant transformations involved the introduction of a marker gene together with a single ICP gene, within the same plasmid, in the plant genome (e.g., Vaeck et al., 1987; Fischoff et al., 1987). Such chimeric ICP genes usually comprised either all or part of an ICP gene, preferably a truncated ICP gene fragment encoding the toxic core, fused to a selectable marker gene, such as the neo gene coding for neomycin phosphotransferase. The chimeric ICP gene was placed between the T-DNA border repeats for Agrobacterium Ti-plasmid mediated transformation (EP 0193259).

This invention involves the combined expression of two or even more B. thuringiensis ICP genes in transgenic plants. The insecticidally effective B. thuringiensis ICP genes, encoding two non-competitively binding ICPs for a target insect species, preferably encoding the respective truncated ICP genes, are inserted in a plant cell genome, preferably in its nuclear genome, so that the inserted genes are downstream of, and under the control of, a promoter which can direct the expression of the genes in the plant cell. This is preferably accomplished by inserting, in the plant cell genome, one or more chimaeric genes, each containing in the same transcriptional unit: at least one ICP gene; preferably a marker gene; and optionally a DNA sequence encoding a protease (e.g., trypsin)-sensitive or -cleavable protein part intercalated in frame between any two ICP genes in the chimaeric gene. Each chimaeric gene also contains at least one promoter which can direct expression of its ICP gene in the plant cell.

The selection of suitable promoters for the chimaeric genes of this invention is not critical. Preferred promoters for such chimaeric genes include: the strong constitutive 35S promoter obtained from the cauliflower mosaic virus, isolates CM 1841 (Gardner et al., 1981), cabbB-S (Franck et al., 1980) and cabbB-JI (Hull and Howell, 1987); the promoter of the nopaline synthetase gene ("PNOS") of the Ti-plasmid (Herrera-Estrella, 1983); the promoter of the octopine synthase gene ("POCS" [De Greve et al., 1982]); and the wound-inducible TR1' promoter and the TR2' promoter which drive the expression of the 1' and 2' genes, respectively, of the T-DNA (Velten et al., 1984). Alternatively, a promoter can be utilized which is specific for one or more tissues or organs of the plant, whereby the inserted genes are expressed only in cells of the specific tissue(s) or organ(s). Examples of such promoters are a stem-specific promoter such as the AdoMet-synthetase promoter (Peleman et al., 1989), a tuber-specific promoter (Rocha-Sosa et al., 1989), and a seed-specific promoter such as the 2S promoter (Krebbers et al., 1988). The ICP genes could also be selectively expressed in the leaves of a plant (e.g., potato) by placing the genes under the control of a light-inducible promoter such as the promoter of the ribulose-1,5-bisphosphate carboxylase small subunit gene of the plant itself or of another plant such as pea as disclosed in EP 0193259. Another alternative is to use a promoter whose expression is inducible (e.g., by temperature or chemical factors).

A 3' non-translated DNA sequence, which functions in plant cells for 3' end formation and the polyadenylation of the 3' end of the mRNA sequence encoded by the at least one ICP gene in the plant cell, also forms part of each such chimeric gene. The selection of a suitable 3' non-translated DNA sequence is not critical. Examples are the 3' untranslated end of the octopine synthase gene, the nopaline synthase gene or the T-DNA gene 7 (Velten and Schell, 1985).

The selection of marker genes for the chimaeric genes of this invention also is not critical, and any conventional DNA sequence can be used which encodes a protein or polypeptide which renders plant cells, expressing the DNA sequence, readily distinguishable from plant cells not expressing the DNA sequence (EP 0344029). The marker gene can be under the control of its own promoter and have its own 3' non-translated DNA sequence as disclosed above, provided the marker gene is in the same genetic locus as the ICP gene(s) which it identifies. The marker gene can be, for example: a herbicide resistance gene such as the sfr or sfrv genes (EPA 87400141); a gene encoding a modified target enzyme for a herbicide having a lower affinity for the herbicide than the natural (non-modified) target enzyme, such as a modified 5-EPSP as a target for glyphosate (U.S. patent 4,535,060; EP 0218571) or a modified glutamine synthetase as a target for a glutamine syn-

thetase inhibitor (EP 0240972); or an antibiotic resistance gene, such as a neo gene (PCT publication WO 84/02913; EP 0193259).

Using A. tumefaciens Ti vector-mediated plant transformation methodology, all chimeric genes of this invention can be inserted into plant cell genomes after the chimaeric genes have been placed between the T-DNA border repeats of suitable disarmed Ti-plasmid vectors (Deblaere et al., 1988). This transformation can be carried out in a conventional manner, for example as described in EP 0116718, PCT publication WO 84/02913 and EPA 87400544.0. The chimeric genes can also be in non-specific plasmid vectors which can be used for direct gene transfer (e.g., as described by Pazkowski et al., 1984; De La Pena et al., 1986). Different conventional procedures can be followed to obtain a combined expression of two B.thuringiensis ICP genes in transgenic plants as summarized below.

I Chimeric gene constructs whereby two or more ICP genes and a marker gene are transferred to the plant genome as a single piece of DNA and lead to the insertion in a single locus in the genome

Ia The genes can be engineered in different transcriptional units each under control of a distinct promoter

To express two or more ICP genes and a marker gene as separate transcriptional units, several promoter fragments directing expression in plant cells can be used as described above. All combinations of the promoters mentioned above in the chimaeric constructs for one ICP gene are possible. Examples of such individual chimeric constructs are described for the bt2 gene in EP 0193259, for the bt13 gene in EPA 88402115.5 and for the bt18 gene in EPA 88402241.9. The ICP gene in each chimeric gene of this invention can be the intact ICP gene or preferably an insecticidally-effective part of the intact ICP gene, especially a truncated gene fragment encoding the toxic core of the ICP. The individual chimeric genes are cloned in the same plasmid vector according to standard procedures (e.g., EP 0193259).

Ib Two genes (e.g., either an ICP and a marker gene or two ICP genes) or more can be combined in the same transcriptional unit

To express two or more ICP genes in the same transcriptional unit, the following cases can be distinguished:

In a first case, hybrid genes in which the coding region of one gene is in frame fused with the coding region of another gene can be placed under the control of a single promoter. Fusions can be made between either an ICP and a marker gene or between two ICP genes. An example of an ICP gene-marker gene fusion has been described in EP 0193259 (i.e., a hybrid truncated bt2-neo gene encoding a Bt2 toxin-NPTII fusion protein).

Another possibility is the fusion of two ICP genes. Between each gene encoding an ICP which still is insecticidally active (i.e., a toxic part of the protoxin), a gene fragment encoding a protease (e.g., trypsin) - sensitive protein part should be included, such as a gene fragment encoding a part of the N-terminal or C-terminal amino acid sequence of one of the ICPs which is removed or cleaved upon activation by the midgut enzymes of the target insect species.

In a second case, the coding regions of the two respective ICP genes can be combined in dicistronic units placed under the control of a promoter. The coding regions of the two ICP genes are placed after each other with an intergenic sequence of defined length. A single messenger RNA molecule is generated, leading to the translation into two separate gene products. Based on a modified scanning model (Kozak, 1987), the concept of reinitiation of translation has been accepted provided that a termination codon in frame with the upstream ATG precedes the downstream ATG. Experimental data also demonstrated that the plant translational machinery is able to synthesize several polypeptides from a polycistronic MRNA (Angenon et al., 1989).

II Chimeric constructs with one or more ICP genes that are transferred to the genome of a plant already transformed with a one or more ICP genes

Several genes can be introduced into a plant cell during sequential transformation steps (retransformation), provided that an alternative system to select transformants is available for the second round of transformation. This retransformation leads to the combined expression of ICP genes which are introduced at multiple loci in the genome. Preferably, two different selectable marker genes are used in the two consecutive transformation steps. The first marker is used for selection of transformed cells in the first transformation, while the second marker is used for selection of transformants in the second round of transformation. Sequential transformation steps using kanamycin and hygromycin have been described, for example by Sandler

et al. (1988) and Delauney et al. (1988).

III Chimeric constructs with one or more ICP genes, that are separately transferred to the nuclear genome of separate plants in independent transformation events and are subsequently combined in a single plant genome through crosses.

The first plant should be a plant transformed with a first ICP gene or an F1 plant derived herefrom through selfing (preferably an F1 plant which is homozygous for the ICP gene). The second plant should be a plant transformed with a second ICP gene or an F1 plant derived herefrom through selfing (preferably an F1 plant which is homozygous for the second ICP gene). Selection methods can be applied to the plants obtained from this cross in order to select those plants having the two ICP genes present in their genome (e.g., Southern blotting) and expressing the two ICPs (e.g., separate ELISA detection of the immunologically different ICPs). This is a useful strategy to produce hybrid varieties from two parental lines, each transformed with a different ICP gene, as well as to produce inbred lines containing two different ICP genes through crossing of two independent transformants (or their F1 selfed offspring) from the same inbred line.

IV Chimeric constructs with one or more ICP genes separately transferred to the genome of a single plant in the same transformation experiment leading to the insertion of the respective chimeric genes at multiple loci.

Cotransformation involves the simultaneous transformation of a plant with two different expression vectors, one containing a first ICP gene, the second containing a second ICP gene. Along with each ICP gene, a different marker gene can be used, and selection can be made with the two markers simultaneously. Alternatively, a single marker can be used, and a sufficiently large number of selected plants can be screened in order to find those plants having the two ICP genes (e.g., by Southern blotting) and expressing the two proteins (e.g., by means of ELISA). Cotransformation with more than one T-DNA can be accomplished by using simultaneously two different strains of Agrobacterium, each with a different Ti-plasmid (Depicker et al., 1985) or with one strain of Agrobacterium containing two T-DNAs on separate plasmids (de Framond et al., 1986). Direct gene transfer, using a mixture of two plasmids, can also be employed to cotransform plant cells with a selectable and a non-selectable gene (Schocher et al., 1986).

The transgenic plant obtained can be used in further plant breeding schemes. The transformed plant can be selfed to obtain a plant which is homozygous for the inserted genes. If the plant is an inbred line, this homozygous plant can be used to produce seeds directly or as a parental line for a hybrid variety. The gene can also be crossed into open pollinated populations or other inbred lines of the same plant using conventional plant breeding approaches.

Of course other plant transformation methods can be used and are within the scope of the invention as long as they result is a plant which expresses two or more non-competitively binding ICPs. In this regard, this invention is not limited to the use of Agrobacterium Ti-plasmids for transforming plant cells with genes encoding non-competitively binding ICPs. Other known methods for plant cell transformations, such as electroporation or by the use of a vector system based on plant viruses or pollen, can be used for transforming monocotyledonous and dicotyledonous plants in order to obtain plants which express two non-competitively binding ICPs. Furthermore, DNA sequences encoding two non-competitively binding ICPs other than those disclosed herein can be used for transforming plants. Also, each of the ICP genes, described herein, can be encoded by equivalent DNA sequences, taking into consideration the degeneracy of the genetic code. Also, equivalent ICPs with only a few amino acids changed, such as would be obtained through mutations in the ICP gene, can also be used, provided they encode a protein with essentially the same characteristics (e.g., insecticidal activity and receptor binding).

The following Examples illustrate the invention. Those skilled in the art will, however, recognize that other combinations of two or more non-competitively binding B. thuringiensis ICP genes can be used to transform plants in accordance with this invention in order to prevent the development, in a target insect, of resistance to B. thuringiensis ICPs expressed in the transformed plants. Unless otherwise indicated, all procedures for making and manipulating DNA were carried out by the standardized procedures described in Maniatis et al, Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory (1982).

EXAMPLE 1: Collection of genes

The collection of anti-Lepidopteran and anti-Coleopteran Bt genes encoding ICPs, which are the subject of the Examples, is described in Table 2 (following the Examples). References for the respective genes are

indicated in Table 2. The origin, the isolation and characterization of the Bt genes, which have not been published, are described below. Bt strains, such as strains HD-1, HD-68, HD-110, and HD-73, are publicly available from the Agricultural Research Culture Collection, Northern Regional Research Laboratory, U.S. Dept. of Agriculture, Peoria, Illinois 61604, U.S.A.

bt3 gene: From B. thuringiensis var. kurstaki HD-1, the ICP was cloned. Characterization of this gene revealed an open reading frame of 3528 bp which encodes a protoxin of 133 kDa. This gene was identical to the one described by Schnepf et al. (1985).

bt73 gene: From B. thuringiensis var HD-73. The ICP gene was cloned as described by Adang et al. (1985).

bt4 gene: A genomic library was prepared from total DNA of strain B. thuringiensis aizawai HD-68. Using the 1.1 kb internal HindIII fragment of the bt2 gene as a probe, a gene designated bt4 was isolated. Characterization of this gene revealed an open reading frame of 3495 bp which encodes a protoxin of 132 kDa and a trypsin activated toxin fragment of 60 kDa. This (insect controlling protein) gene differs from previously identified genes and was also found in several other strains of subspecies aizawai and entomocidus including HD-110. Fig. 13 shows the nucleotide sequence and deduced amino acid sequence of the open reading frame ("ORF") of the bt4 gene extending from nucleotide 264 to nucleotide 3761.

bt 14 and bt15 genes: A genomic library was prepared from total DNA of strain B. thuringiensis var. entomocidus HD-110 by partial Dau3A digest of the total DNA and cloning in the vector pEcoR251 (deposited at DSM under accession number 4711). Using monoclonal antibodies (Höfte et al., 1988), at least three structurally distinct ICPs were identified in crystals of B. thuringiensis entomocidus HD-110. These monoclonal antibodies were used to clone the three different ICP genes from this B. thuringiensis strain. One of these genes is the bt4 gene as described above.

The second gene was called "bt15". Fig. 14 shows the nucleotide sequence and deduced amino acid sequence of the ORF of the bt15 gene, isolated from HD-110, extending from nucleotide 234 to nucleotide 3803. The Shine and Dalgarno sequence, preceding the initiation codon is underlined. This gene has an open reading frame of 3567 bp which encodes a protoxin of 135 kDa and a 63 kDa toxin fragment. A similar gene has been described by Honee et al. 1988, isolated from B. thuringiensis entomocidus 60.5. The bt15 gene differs from the published sequence at three positions: an Ala codon (GCA) is present instead of an Arg codon (CGA) at position 925 and a consecution of a Thr-His codon (ACGCAT) is present instead of a Thr-Asp codon (ACCGAT) at position 1400. (The numbers of the positions are according to Honnee et al., 1988). Another similar gene has been described in EP 0295156, isolated from B. thuringiensis aizawai 7-29 and entomocidus 6-01. The bt15 gene is different from this published nucleotide sequence at three different places : 1) a Glu codon (GAA) instead of an Ala codon (GCA) at position 700; 2) the sequence TGG, CCA, GCG, CCA instead of TGC, CAG, CGC, CAC, CAT at position 1456 and 3) an Arg codon (CGT) instead of an Ala codon (GCG) at position 2654. (The numbers of the positions are according to EP 0295156).

The third gene isolated was called "bt14". It has an open reading frame of 3621 bp which encodes a 137 kDa protoxin and a 66 kDa activated toxin fragment. A similar gene has been cloned from B.thuringiensis HD-2 (Brizzard and whiteley, 1988). The bt14 gene differs from the published nucleotide sequence by two nucleotide substitutions: a T instead of a C at position 126, and a C instead of a T at position 448 (the numbers of the positions are according to Brizzard and Whiteley, 1988). In the first case, the Ile codon (ATT or ATC) is conserved whereas in the second case the Tyr codon (TAT) is converted to a His codon (CAC).

bt2 gene: The bt2 gene was cloned as described in EP 0193259.

bt18 gene: Cloning of the bt18 gene was performed as described in EPA 88402241.9.

bt13 gene: The bt13 gene was cloned as described in EPA 88402115.5.

bt21 and bt22 genes: These genes, encoding Coleopteran-active ICPs, were cloned as described in EPA 89400428.2.

EXAMPLE 2 : Construction of gene cassettes and expression of Bt genes in E.coli

1) bt2, bt18: the construction of bt2 and bt18 gene cassettes has been previously described in EPA 86300291.1 and 88402241.9, respectively. Basically, they comprise a truncated gene encoding the toxic core and a hybrid gene comprising the truncated gene fused in frame to the N-terminus of the neo gene. The gene cassettes are used to transform E. coli to express the Bt2 and Bt18 ICP toxins.

2) bt14, bt15: as described in EPA 88402241.9, gene cassettes for the bt14 and bt15 genes were constructed in order to express the genes in E.coli and in plants.

First, a NcoI site was introduced at the N-terminus of the genes by site-directed mutagenesis.

In the case of the bt15 gene, the conversion of the TT nucleotides, immediately in front of the ATG codon, into CC yielded a NcoI site overlapping with the ATG initiation codon. This site was introduced using the pMa/c vectors for site-directed mutagenesis (Stanssens et al., 1987) and a 28-mer oligonucleotide with the following sequence:

5'-CGGAGGTATTCCATGGAGGAAAATAATC-3'.

This yielded the plasmid pVE29 carrying the N-terminal fragment of the bt15 gene with a NcoI site at the ATG initiation codon.

According to Brizzard and Whiteley (1988), the initiation codon of the bt14 gene is a TTG codon. Thus, a NcoI site was created in a like manner at this codon for site directed mutagenesis using a 34-mer oligonucleotide with the following sequence :

5'-CCTATTTGAAGCCATGGTAACTCCTCCTTTTATG-3'.

In this case the sequence of the intitiation codon was converted from ATATTGA to ACCATGG. This yielded the plasmid pHW44 carrying the N-terminal fragment of the bt14 gene with a NcoI site at the initiation codon.

In a second step, the genes were reconstructed by ligating the N-terminal gene fragments with a suitable C-terminal gene fragment, yielding a bt15 gene and bt14 gene with a NcoI site at the ATG initiation codon.

To express the bt14 and bt15 genes encoding the protoxin in E. coli, the following constructs were made: POH50 containing the bt15 gene under the control of the lac promoter; and pHW67 containing the bt14 gene under the control of the tac promoter. Induction of a culture of the E. coli strain WK6 carrying the respective plasmids with IPTG yielded an overproduced protein (Fuller, 1982).

The active toxic fragments of the Bt15 and Bt14 protoxins comprise 63 and 60 kDa trypsin digest products respectively. Instead of expressing the whole bt15 or bt14 gene, it is also possible to express a toxin-encoding gene fragment or derivative thereof in plants. To this end, truncated bt14 and bt15 gene fragments were constructed. In order to be able to select transgenic plants producing the ICP gene products, hybrid genes of the truncated gene fragments were also made with the neo gene encoding a selectable marker as described in EP 0193259.

By comparison of the nucleotide sequence of the bt4, bt14 and bt15 genes, respectively, with the bt2 and bt18 genes, respectively, the BclI site could be identified as a suitable site localized downstream of the coding sequence encoding the toxin gene fragment. To construct a truncated gene fragment and a hybrid gene of the truncated gene fragment with the neo gene, the filled BclI site was ligated to the filled EcoRI site of pLKM91 (Höfte et al., 1986) and the filled HindIII site of pLK94 respectively (Botterman and Zabeau, 1987). pLKM91 carries a 5' truncated neo gene fragment which codes for an enzymatically active C-terminal gene fragment of the neo gene, and pLK94 contains translation stop codons in three reading frames. This yielded the following plasmids which are then used to transform E. coli to express the ICP genes: pHW71 carrying a truncated bt14-neo hybrid gene; pHW72 carrying a truncated bt14 gene; pVE34 carrying a truncated bt15-neo hybrid gene; and pVE35 carrying a truncated bt15 gene.

In a similar way as described for the bt14 and bt15 genes, gene cassettes are constructed for the bt3 and bt4 genes which are then expressed in E.coli.

EXAMPLE 3: Purification of recombinant ICPs

The ICPs expressed in E. coli in Example 2 are purified by the method (described for recombinant Bt2 protoxin) by Höfte et al. (1986).

EXAMPLE 4: Purification of toxins

Solubilized protoxins of Bt2, Bt3, Bt73, Bt4, Bt14, Bt15, Bt18, Bt13, Bt21 and Bt22 (in Na_2CO_3 50mM, DTT 10 mM pH=10) are dialyzed against 0.5 % $(NH_4)_2CO_3$ at pH 8 and treated with trypsin (trypsin/protoxin=1/20 w/w) for 2h at 37°C. The activated toxin is chromatographically purified (Mono-Q column on FPLC) as described by Hofmann et al.(1988b).

EXAMPLE 5: Determination of the insecticidal spectrum

The ICP protoxins and toxins of Examples 3 and 4 are evaluated for their insecticidal activity. Each protoxin

is dissolved in alkaline buffer containing a reducing agent (Na_2CO_3 50 mM, DTT 10 mM pH=10), and each toxin is used as soluble protein directly from FPLC. Protein concentrations are determined. Subsequently, dilutions of the resulting protoxin or toxin solution are prepared in PBS buffer pH=7.4 containing 0.15 M NaCl and 0.1 % bovine serum albumin ("BSA").

The artificial medium for insect culture, described by Bell and Joachim (1976) for Manduca sexta, is poured in appropriate receptacles and allowed to solidify. Subsequently a quantity of the (pro) toxin dilutions is applied on this medium, and the water is allowed to evaporate under a laminar flow. This results in a medium with a certain quantity (in the range of 0.1 to 10000 ng/cm2) of toxin coated on its surface. For example, for the Bt2 toxin, typical dilutions for a toxicity test on Manduca sexta are 1, 5, 25, 125 and 625 ng/cm^2. First instar larvae of Manduca sexta are then applied on the coated medium, and growth and mortality are assessed after 6 days. Mortality increases with dosage. Dose response data is analysed in probit analysis (Finney, 1962), and the data are best summarized by an LD_{50} value which is the amount of toxin which kills 50 % of the insects. The LD_{50} for Bt2 toxin against Manduca sexta is around 20 ng/cm2.

Similar assays are carried out for other insect species using a suitable diet or by applying the ICPs on leaves for insects, for which no artificial diet is used.

EXAMPLE 6: Binding studies

Toxins

All protoxins and their toxic fragments were purified according to the methods described for the Bt2 protoxin and toxin in Höfte et al. (1986) and EP 0193259. The activated and purified toxins are further referred to as the Bt2, Bt3, Bt73, Bt4, Bt14, Bt15, Bt18, Bt13, Bt21 and Bt22 toxins.

By way of example for the Bt73 toxin, it has been shown that B. thuringiensis var. kurstaki HD73 produces a protein of 133 kDa encoded by a 6.6 kb type gene. A culture of this strain was grown as described by Mahillon and Delcour (1984). The autolysed culture was spun down (20 minutes at 4500 rpm in a HB4 rotor) and washed with a buffer containing 20 mM Tris, 100 mM NaCl and 0.05 % Triton X-100, pH 8. The final pellet was resuspended in this buffer (4 ml buffer for 100 ml culture). This solution was then layered onto a linear Urograffin gradient (60-70%) which was centrifuged in a SW 28 rotor for 90 minutes at 18000 rpm. Crystals were collected and stored at -20°C until further use. Activation was performed according to Höfte et al. (1986). The purified toxin is further referred to as the Bt73 toxin.

Iodination of ICPs

Iodination of Bt2, Bt3, and Bt73 toxins was performed using the Chloramin-T method (Hunter and Greenwood, 1962). 1 mCi ^{125}I-NaI and 20 to 37.5 ug Chloramin-T in NaCl/P_i were added to 50 ug of purified toxin. After gentle shaking for 60 seconds, the reaction was stopped by adding 53 ug of potassium metabisulfite in H_2O. The whole mixture was loaded on a PD 10 Sephadex G-25M gelfiltration column to remove free iodine. A subsequent run on a Biogel P-60 column was carried out in order to increase the purity.

Alternatively, toxins were labeled using the Iodogen method. Iodogen (Pierce) was dissolved in chloroform at 0.1 mg/ml. 100 ul of this solution was pipetted into a disposable glass vessel and dried under a stream of nitrogen gas. The vessel was rinsed with Tris buffer (20 mM Tris, pH 8.65 with 0.15 M NaCl). 50 ug of toxin (in Tris buffer) was incubated with 1 mCi of ^{125}I-NaI in the tube for 10 minutes. The reaction was then stopped by the addition of 1 M NaI (one fourth of the sample volume). The sample was immediately loaded onto a PD10 Sephadex G-25M column and later on a Biogel P-60 column to remove free iodine and possible degradation products.

Other toxins were iodinated using one of the above mentioned procedures.

Determination of specific activity of iodinated toxin

Specific activity of iodinated Bt2, Bt3, and Bt73 toxin samples was determined using a "sandwich" ELISA technique according to Voller, Bidwell and Barlett (1976). Primary antibody was a polyclonal antiserum raised against Bt2 toxin, and the secondary antibody was a monoclonal antibody 4D6.

The conjugate used was alkaline phosphatase coupled to anti-mouse IgG. The reaction intensity of a standard dilution series of unlabeled toxin and dilutions of the iodinated toxin sample (in NaCl/P_i - 0.1 % BSA) was measured. Linear regression calculations yielded the protein content of the radioactive toxin sample. The samples with the highest specific activities were used in the binding assays. Specific activities were 59400, 33000 and 19800 Ci/mole (on reference date) for Bt73 toxin (labeled according to Iodogen procedure), Bt2 toxin (Chlor-

amin-T method) and Bt3 toxin (Iodogen method) respectively.

Specific activities of other toxins were determined using a similar approach. Specific monoclonal and polyclonal antibodies for each of these toxins were raised and applied in ELISA.

Preparation of brush border membrane vesicles

Brush border membrane vesicles ("BBMV") from Manduca sexta, Heliothis virescens, Plutella xylostella, Phthorimaea operculella, Spodoptera exigua, Spodoptera littoralis, Plodia interpunctella, Mamestra brassicae, Pieris brassicae and Leptinotarsa decemlineata were prepared according to the method of Wolfersberger et al. (1987). This is a differential centrifugation method that makes use of the higher density of negative electrostatic charges on luminal than on basolateral membranes to separate these fractions.

Binding assay

Duplicate samples of ^{125}I-labeled toxin, either alone or in combination with varying amounts of unlabeled toxin, were incubated at the appropriate temperature with brush border membrane vesicles in a total volume of 100 ul of Tris buffer (Tris 10 mM, 150 mM NaCl, pH 7.4). All buffers contained 0.1 % BSA. The incubation temperature was 20 C. Ultrafiltration through Whatman GF/F glass fiber filters was used to separate bound from free toxin. Each filter was rapidly washed with 5 ml of ice-cold buffer (NaCl/P_i- 0.1 % BSA). The radioactivity of the filter was measured in a gammacounter (1275 Minigamma, LKB). Binding data were analyzed using the LIGAND computer program. This program calculates the bound concentration of ligand as a function of the total concentration of ligand, given the affinity (Ka or its inverse Kd = 1/Ka, the dissociation constant) and the total concentration of receptors or binding site concentration (R_t).

Determination of protein concentration

Protein concentrations of purified Bt2, Bt3, Bt73 and Bt15 toxins were calculated from the OD at 280 nm (measured with a Uvikon 810 P, Kontron Instruments spectrofotometer). The protein content of solutions of other toxins and of brush border membrane vesicles (BBMV) as measured according to Bradford (1976).

Binding of Bt2, Bt3 and Bt73 toxins to 88MV of Manduca sexta and Heliothis virescens: an example of 3 competitively binding Lepidopteran ICPs.

Bt2, Bt3 and Bt73 toxins are toxic to both Manduca sexta and Heliothis virescens: LC50 values for Manduca sexta are respectively 17.70, 20.20 and 9.00 ng/cm2 ; for Heliothis virescens the LC50's are 7.16, 90.00 and 1.60 ng/cm2.

Labelled toxin, either Bt3 (0.8 nM) or Bt2 (1.05 nM) or Bt73 (1.05 nM), was incubated with BBMV in a volume of 0.1 ml. BBMV protein concentrations were 100 ug/ml for M. sexta and for Bt2-H. virescens, for Bt3-H. virescens 150 and for Bt73-H. virescens 50 ug/ml. The labelled toxin was combined with varying amounts of an unlabeled toxin (competitor). After a 30 min. incubation, bound and free toxins were separated through filtration.

Figs. 1-3 show the percentages binding of respectively labelled Bt2, Bt3 and Bt73 toxins as a function of the concentration of competitor for Manduca sexta. Figs. 4-6 show these data for Heliothis virescens. The amount bound in the absence of competitor is always taken as 100 % binding. Figs. 1-6 show the binding of ^{125}I-labeled toxins to M. sexta (in Figs. 1, 2 and 3) and H. virescens (in Figs. 4, 5 and 6) brush border membrane vesicles. Vesicles were incubated with labeled toxin [in Figs. 1 and 4: ^{125}I-Bt2-toxin (1.05nM); in Figs. 2 and 5: ^{125}I-Bt3-toxin (0.8nM); in Figs. 3 and 6: ^{125}I-Bt73-toxin (1.05nM)] in the presence of increasing concentrations of Bt2 toxin (*), Bt3 toxin (●) or Bt73 toxin (▲). Binding is expressed as percentage of the amount bound upon incubation with labeled toxin alone. On M. sexta vesicles, these amounts were 1820, 601 and 2383 cpm, and on H. virescens vesicles 1775, 472 and 6608 cpm for ^{125}I-Bt2-, Bt3- and Bt73-toxin, respectively. Non-specific binding was not substracted. Data were analyzed with the LIGAND computer program. Each point is the mean of a duplicate sample.

Figure 1: shows the binding of ^{125}I Bt2 toxin to M. sexta BBMV
Figure 2: shows the binding of ^{125}I Bt3 toxin to M. sexta BBMV
Figure 3: shows the binding of ^{125}I Bt73 toxin to M. sexta BBMV
Figure 4: shows the binding of ^{125}I Bt2 toxin to H. virescens BBMV
Figure 5: shows the binding of ^{125}I Bt3 toxin to H.virescens BBMV
Figure 6: shows the binding of ^{125}I Bt73 toxin to H.virescens BBMV

The conclusions from Figures 1-6 are that Bt2 and Bt3, Bt3 and Bt73, and Bt2 and Bt73 are competitively-binding ICP's both for Manduca sexta and for Heliothis virescens. Indeed Bt3 competes for the entire population of receptor sites of Bt2 in Manduca sexta (Fig.1): the % labelled Bt2 bound in the presence of 100 nM Bt3 is equal to the % Bt2 bound with 100 nM of Bt2 itself. The opposite is not true: in the presence of 100 nM Bt2 the % of labelled Bt3 is not reduced to the same level as with 100 nM of Bt3 (Fig.2).

A similar reasoning is followed to observe competitivity of other toxin combinations : Bt3 competes for the entire population of receptor sites of Bt73 (Fig. 3) in M. sexta; the opposite is not true (Fig. 2); Bt2 and Bt73 compete for the entire population of each other's binding sites in M. sexta (Figs. 1 and 3).

In Heliothis virescens : Bt2 competes for the entire population of receptor sites of Bt3 (Fig. 5); Bt73 competes for the entire population of receptor sites of Bt3 (Fig. 5); Bt73 competes for the entire population of receptor sites of Bt2 (Fig. 4); but the opposite statements are not true (Figs. 4, 5 and 6).

The same data can be used in mathematical analysis (e.g., Scatchard analysis according to Scatchard, 1949; analysis with the LIGAND computer program according to Munson and Rodbard, 1980) to calculate the dissociation constant (Kd) of the toxin-receptor complex and the concentration of binding sites (Rt); the results of these calculations using the LIGAND computer program were the following:

Bt2-M.sexta:	Kd=0.4 nM	Rt=3.4 pmol/mg vesicle protein
Bt3-M. sexta:	Kd=1.5 nM	Rt=9.8 pmol/mg vesicle protein
Bt73-M. sexta:	Kd=0.6 nM	Rt=4.0 pmol/mg vesicle protein
Bt2-H. virescens:	Kd=0.6 nM	Rt=9.7 pmol/mg vesicle protein
Bt3-H. virescens:	Kd=1.2 nM	Rt=3.7 pmol/mg vesicle protein
Bt73-H. virescens:	Kd=0.8 nM	Rt=19.5 pmol/mg vesicle protein

These data demonstrate the high affinity receptor binding of the toxins (Kds in the range of 10^{-10} to 10^{-9} M.

Binding of Bt2 and Bt14 toxins to BBMV of P. brassicae Plutella xylostella and Phthorimaea operculella: an example two non-competitively binding Lepidopteran ICPs

Bt2 and Bt14 toxins are toxic to P. brassicae (p.b.), P. xylostella (p.x.) and P. operculella (p.o.) as seen from the table below.

	LC_{50} of Toxins	
	Bt2	Bt14
P.b.	1.3	2.0
P.x.	6.7	5.4
P.o.	4.20	0.8-4.0

LC_{50} values of solubilized purified Bt2 and Bt14 toxins for P.x. are expressed as ng protein spotted per cm^2 of artificial diet. LC_{50} values for P.b. are expressed as ug^2 toxin per ml solution into which leaf discs, fed to first instar Pb larvae, were dipped. For P.o., LC_{50} values are expressed in ug/ml into which potato chips were dipped prior to feeding.

Labelled Bt2 toxin (1.05 nM) or Bt14 toxin (1.4 nM) was incubated with BBMV from P. brassicae (100 ug protein/ml) in a volume of 0.1 ml in combination with varying amounts of unlabelled Bt2 or Bt14. After a 30 min. incubation period at 22°C, the bound and free toxins were separated.

Figures 7 and 8 show the binding of ^{125}I-labeled toxins to P. brassicae brush border membrane vesicles. Vesicles were incubated with labeled toxin [in Fig. 7: ^{125}I-Bt2-toxin (1.05nM) in Fig. 8: ^{125}I-Bt14-toxin (1.4nM)] in the presence of increasing concentrations of Bt2 toxin (o) or Bt14 toxin (●). Binding is expressed as percentage of the amount bound upon incubation with labeled toxin alone. Non-specific binding was not substracted. Data were analyzed with the LIGAND computer program. Each point is the mean of a duplicate sample. Figure 7 shows the binding of labelled Bt2 toxin to P. brassicae BBMV, and Figure 8 shows the binding of labelled Bt14 toxin to P. brassicae BBMV.

The competition data demonstrate the presence of high affinity binding sites both for Bt2 and Bt14, as well as the almost complete absence of competition of Bt14 for the Bt2 binding sites and of Bt14 for the Bt2 binding sites. This demonstrates that Bt2 and Bt14 are non-competitively binding toxins. Hence they are useful to prevent the development of Pieris brassicae resistance against B. thuringiensis ICP's expressed in Brassica sp.

Calculated Kd and Rt values were from these experiments were:
Bt2: Kd=2.8 nM, Rt=12.9 pmol/mg vesicle protein
Bt14: Kd=8.4 nM, Rt=21.4 pmol/mg vesicle protein.

Binding of Bt2 and Bt15 toxins to BBMV of M.sexta, M.brassicae, P. xylostella and P.interpunctella : an example of two non-competitively binding Lepidopteran ICPs

Bt2 and bt15 toxins are both toxic to M.sexta (LC50's of 20 and 111 ng/cm^2, respectively). They also show activity against M. brassicae, P. xylostella and P. interpunctella.

Labelled Bt2 (1.05 nM) or Bt15 (0.7 nM) was incubated with BBMV from M.sexta (100 ug protein/ ml) in a volume of 0.1 ml in combination with varying amounts of unlabelled Bt2 or Bt15. After a 30 min. incubation period at 22°C, the bound and free toxins were separated.

Figs. 9-10 show the binding of ^{125}I-labeled toxins to M. sexta brush border membrane vesicles. Vesicles were incubated with labeled toxin [in Fig. 9: ^{125}I-Bt2-toxin (1.05nM); in Fig. 10: ^{125}I-Bt15-toxin (0.7nM)] in the presence of increasing concentrations of Bt2-toxin (o) or Bt15-toxin (●). Binding is expressed as percentage of the amount bound upon incubation with labeled toxin alone. Non-specific binding was not substracted. Data were analyzed with the LIGAND computer program. Each point is the mean of a duplicate sample. Figure 9 shows the data for binding of labelled Bt2, and Figure 10 shows the binding of labelled Bt15.

The competition data demonstrate the presence of high affinity binding sites for both Bt2 and Bt15, as well as the complete absence of competition of Bt15 for the Bt2 binding sites and of Bt2 for the Bt15 binding sites. This demonstrates that Bt2 and bt15 are non-competitively binding toxins. Hence the combination of Bt2 and Bt15 is useful to prevent the development of resistance of M.sexta against B. thuringiensis ICP's expressed in tobacco or other crops in which Manduca sp. are a pest. Calculated Kd and Rt values are:
Bt2: Kd=0.4 nM, Rt=3.4 pmol/mg vesicle protein Bt15: Kd = 0.3 nM Kd2=2.9 nM, Rt1= 5.9 and Rt2=6.7 pmol/mg vesicle protein (2 distinct high affinity receptor sites are present).

Similar studies were performed for M. brassicae, S. littoralis and P. interpunctella. Although LD50, Kd and Rt values differed substantially, the essential observation that Bt2 and Bt15 are both toxic and are non-competitively binding toxins was confirmed in these three insect species. Thus, it is also a useful toxin combination to prevent resistance of M. brassicae to ICP's or to prevent resistance of Spodoptera species against ICP's expressed in any of the crop plants in which Spodoptera species are a pest.

Binding of Bt2 and Bt4 toxins to BBMV of M. sexta: an example of two non-competitively binding Lepidopteran ICPs

Both Bt2 and Bt4 toxins are toxic to Manduca sexta. LD50 values are 20 and 5.4. ng/cm2, respectively. No mutual competition of Bt2 for binding of labelled Bt4 and of Bt4 for binding of labelled Bt2 was observed, demonstrating that Bt2 and Bt4 are non-competitively binding toxins.

Binding of Bt15 and Bt18 toxins to BBMV of S. littoralis: an example of two non-competitively binding Lepidopteran ICPs

Both Bt15 and Bt18 toxins are toxic to S. littoralis. LD 50 values are 93 and 88 ng toxin/cm^2, respectively. Labelled Bt15 (0.7 nM) or Bt18 (0.9 nM) was incubated with 100 ug of vesicle protein from S. littoralis in com-

bination with varying amounts of unlabelled Bt15 or Bt18 toxin. After a 45 min. incubation period, bound and free toxins were separated. Binding data demonstrate high affinity binding for both Bt15 and Bt18 to S. littoralis BBMV. As seen from Figures 11 and 12, the entire population of receptor sites of Bt15 was not saturable with Bt18, nor was the entire population of receptor sites of Bt18 saturable with Bt15.

Binding of Bt13 and Bt22 toxins to BBMV of L. decemlineata : an example of two non-competitively binding Coleopteran ICPs.

Both Bt13 and Bt22 toxins are toxic to L. decemlineata. LD 50 values are 0.8 and 1.1 ug toxin/ml respectively. Labelled Bt13 (1 nM) or Bt22 (0.7 nM) was incubated with 100 ug of vesicle protein/ml from S. littoralis in combination with varying amounts of unlabelled Bt13 or Bt22 toxin. After a 45 min. incubation period, bound and free toxins were separated. Binding data demonstrate high affinity binding for both Bt13 and Bt22 to S. littoralis BBMV. The entire population of receptor sites of Bt13 was not saturable with Bt22. Nor was the entire population of receptor sites of Bt22 saturable with Bt13.

Binding of Bt2 and Bt18 toxins to BBMV of M. sexta: an example of two non-competitively binding Lepidopteran ICPs.

Both Bt2 and Bt18 toxins are toxic to M. sexta, and LD 50 values are 20 to 73 ng toxin/cm^2 respectively. Labelled Bt2 (1.05nM) or Bt18 (0.7nM) was incubated with 100 ug/ml of vesicle protein from M. sexta in combination with varying amounts of unlabelled Bt2 or Bt18 toxin. After a 45 min. incubation period, bound and free toxins were separated. Binding data (Figs. 11-12) demonstrate high affinity binding for both Bt2 and Bt18 to M. sexta BBMV. The entire population of receptor sites of Bt2 was not saturable with Bt18. Nor was the entire population of receptor sites of Bt18 saturable with Bt2. Calculated Kd and Rt values are:
Bt2: Kd= 0.4 nM, Rt= 3.4 pmol/mg vesicle protein. Bt18: Kd1= 0.04 nM, Rt1= 2.2 pmoles/mg vesicle protein and Kd2= 168nM Rt2= 194 pmoles/mg vesicle protein (2 distinct receptor sites for Bt18 are present).

A list of non-competitively binding anti-Lepidopteran ICP combinations and anti-Coleopteran ICP combinations is given below, together with their common target insect species in which non-competitivity has been demonstrated:

Bt2-Bt15 (Manduca sexta, Plutella xylostella, Pieris brassicae, Mamestra brassicae, Plodia interpunctella)
Bt2-Bt18 (Manduca sexta, Spodoptera littoralis)
Bt2-Bt14 (Pieris brassicae, Plutella xylostella, Phthorimaea operculella)
Bt2-Bt4 (Manduca sexta)
Bt15-Bt18 (Manduca sexta, Spodoptera littoralis)
Bt14-Bt15 (Pieris brassicae)
Bt15-Bt4 (Manduca sexta, Spodoptera exigua)
Bt18-Bt4 (Manduca sexta, Spodoptera littoralis)
Bt18-Bt14 (Pieris brassicae)
Bt18-Bt4 (Manduca sexta)
Bt13-Bt21 (Leptinotarsa decemlineata)
Bt13-Bt22 (Leptinotarsa decemlineata)
Bt21-Bt22 (Leptinotarsa decemlineata)

Of course, this list of specific non-competitively binding ICP combinations for specific target insect pests is not exhaustive, and it is believed that other such ICP combinations, including combinations for yet-to-be discovered ICPs, will be found using a similar approach for any target insect species. Likewise, the foregoing list of target insect pests also is not exhaustive, and it is believed that other target insects pests (as well as the plants that are to be transformed to prevent their attack by such pests), against which the specific combinations of ICPs can be used (e.g., the combination of the Bt2 and Bt14 ICPs in Brassica to prevent resistance of Pieris brassicae against the ICPs expressed in the plant), will be found using a similar approach.

EXAMPLE 7: Selection for resistance of Manduca sexta (tobacco hornworm)

A selection experiment involves exposing a large number of larvae to a concentration of a toxin in a diet killing (e.g., 50-90 %) of the larvae. The surviving larvae are again exposed to toxin concentrations killing a similar proportion of the larvae, and this process is continued for several generations. The sensitivity of the larvae to the toxin is investigated after each four generations of selection.

Selections for 20 generations of M. sexta were performed with Bt2 toxin alone, with Bt18 toxin alone and

with a 1/4 (by weight) Bt2/Bt18 mixture. LC50 values of the reference strain for Bt2, Bt18 and the 1/4 Bt2/Bt18 mixture respectively were the following : 20 ng/cm2, 73 ng/cm2 and 62 ng/cm2 of diet.

Selection was initiated at concentrations killing around 75 % of the larvae. After 4 generations of selection, survival increased in both the Bt2 and the Bt18 selection to around 70 %, no such increase was observed in the selection with the combination of Bt2 and Bt18. Dosages were again increased to calculated LC75 values. This was repeated every 4 generations. The selection process was thus continued to the 20th generation. Final results were the following (LC50 of the 20th generation):

- Bt2 selection: LC50 was 6400 ug/g (320 times decreased sensitivity)
- Bt18 selection: LC50 was 15100 ug/g (207 times decreased sensitivity)
- Bt2/Bt18 selection: LC50 was 181 ug/g (3 times decreased sensitivity).

Thus the decrease in sensitivity was about 100 times slower in the combined selection experiment.

Receptor binding in the three selected M. sexta strains was investigated with Bt2 and Bt18 and compared to those of the reference M. sexta strain (non-selected strain). Binding characteristics of the reference strain for the Bt2 and Bt18 toxins were:

Bt2: Kd = 0.4 nM, Rt=3.4 pmol/mg vesicle protein

Bt18: Kd1=0.04 nM, Rt1=2.2 pmoles/mg vesicle protein and Kd2=168nM, Rt2=194 pmoles/mg vesicle protein (2 distinct receptor sites for Bt18 are present).

Figures 11 and 12 show the binding of ^{125}I-labeled toxins to M. sexta brush border membrane vesicle. Vesicles were incubated with labeled toxin [in Fig. 11: ^{125}I-Bt2-toxin (1.05nM); in Fig. 12: ^{125}I-Bt18-toxin (0.7nM)] in the presence of increasing concentrations of Bt2-toxin (o) or Bt18-toxin (●). Binding is expressed as percentage of the amount bound upon incubation with labeled toxin alone. Non-specific binding was not substracted. Data were analyzed with the LIGAND computer program. Each point is the mean of a duplicate sample.

The Bt2 selected strain showed no detectable high affinity binding of Bt2 whereas its Bt18 binding characteristics remained close to the reference strain. (Bt18: Kd1=0.03 nM, Rt1=2.8 pmoles/mg vesicle protein and Kd2=199nM, Rt2=109 pmoles/mg vesicle protein; 2 distinct receptor sites for Bt18 are still present).

The Bt18 selected strain lost the high affinity receptor site for Bt18. The lower affinity site for Bt18 was still present in lower concentration than in the reference strain (Kd=189 nM, Rt=43 nM). Bt2 binding site concentration increased markedly compared to the reference strain (Kd=0.4 nM, Rt=20.8 pmoles/mg vesicle protein). This strain had a Bt2 sensitivity of LC_{50}=4 ng/cm^2. Thus, its sensitivity for Bt2 had increased as compared to the reference strain (LC_{50}=20 ng/cm^2).

The Bt2/Bt18 selected strain showed a slight but statistically non-significant decrease in Bt18 binding site concentration. (Bt2 : Kd = 0.4 nM, Rt=3.4 pmol/mg vesicle protein, Bt18 : Kd1=0.04 nM, Rt1=1.0 pmoles/mg vesicle protein and Kd2=168nM, Rt2=194 pmoles/mg vesicle protein; 2 distinct receptor sites for Bt18 are present). These data demonstrate that, in the two selection lines where resistance occurred, the mechanism was situated at the receptor level. Changes in receptor site are shown to be the most likely mechanism of resistance to B. thuringiensis ICPs.

EXAMPLE 8: Mechanism of resistance of the diamondback moth to the microbial insecticide Bacillus thuringiensis.

The mechanism of development of insect resistance to Icps has been investigated in a P. xylostella strain ("PxR"). This insect strain has developed a high level of resistance in the field against Dipel. Crystals of Dipel preparations contain a mixture of ICPs such as Bt3, Bt2 and Bt73 ICPs; in Example 6, it has been shown that these toxins are competitively binding ICPs.

Resistance to Dipel was confirmed by the toxicity data for the sensitive strain ("PxS") and for the Dipel-resistant strain ("PxR"). High levels of resistance are also observed for the Bt2 protoxin and toxin as shown in the following table :

	LC_{50} of Strains	
	PxS	PxR
Bt2	6.7	> 1350
Bt15	132.6	120.4

LC_{50} data are expressed as ng protein spotted per cm^2 of artificial diet.

However, insect toxicity data show that there is no resistance to the Bt15 protoxin and Bt15 toxin; this ICP

is not present in Dipel crystals. To investigate whether a change in toxin-membrane binding was responsible for resistance, receptor binding studies were performed with ^{125}I-labeled Bt2 toxin and Bt15 toxin, with BBMV derived from larvae midguts of the PxR and PxS strains. The results are summarized in Table 1, below.

ICP	strain	Kd (nM)	Rt (pmol/ mg protein)
Bt2 toxin	PxS	8.1	1.6
	PxR	no binding detectable	
Bt15 toxin	PxS	1.9	4.2
	PxR	3.7	5.8

Table 1 shows that there was high-affinity saturable binding of the Bt2 toxin to midgut membranes of the PxS strain, but the PxR strain showed no detectable level of Bt2 toxin binding. With the Bt15 toxin, there was significant binding to BBMW of both the PxR and PxS strains, and values are not significantly different for the two strains.

These data show that resistance in P. xylostella is due to an alteration in toxin-membrane binding. Resistance to the Bt2 toxin and the sensitivity toward the Bt15 toxin of the PxR strain is reflected by the binding characteristics shown in Table 1.

Hence, when different non-competitively binding ICPs (i.e., Bt2 and Bt15) are available with activity against the same insect species (e.g., P. xylostella), resistance to one ICP(Bt2) does not imply resistance against other ICPs (such as Bt15). Thus, ICPs with different binding properties can be used in combination to delay development of insect resistance to ICPs.

EXAMPLE 9: Separate transfer of two ICP genes within individual transcriptional units to the genome of plant cells

Two procedures are envisaged for obtaining the combined expression of two ICP genes, such as the bt2 and bt15 genes in transgenic plants, such as tomato plants. These procedures are based on the transfer of two chimeric ICP genes, not linked within the same DNA fragment, to the genome of a plant of interest.

A first procedure is based on sequential transformation steps in which a plant, already transformed with a first chimeric ICP gene, is retransformed in order to introduce a second ICP gene. The sequential transformation makes use of two different selectable marker genes, such as the resistance genes for kanamycin ("km") and phosphinotricin acetyl transferase ("PPT"), which confers resistance to phoshinotricin. The use of both these selectable markers has been described in De Block et al. (1987).

The second procedure is based on the cotransformation of two chimeric ICP genes on different plasmids in a single step. The integration of both ICP genes can be selected by making use of the two selectable markers conferring resistance to Km and PPT, linked with the respective ICP genes.

For either procedure, a Ti-plasmid vector is used for Agrobacterium-mediated transformation of each chimeric ICP gene into plant cells.

Plasmid PGSH163, described in EP 0193259, contains the following chimeric genes between the T-DNA border repeats: a gene fragment encoding the toxin part of the bt2 gene under the control of the TR2' promoter and the neo gene under control of the TR1' promoter. The 3' ends of the T-DNA gene 7 and octopine synthase respectively provide information for the 3' end formation of transcripts.

A chimeric bt15 gene containing a gene fragment encoding the toxin of the Bt15 ICP under the control of the TR2' promoter, was constructed in the following way (Figure 15). pOH50 consists of pUC18 with the whole bt15 gene under the control of the lac promoter. A HindIII-BglII fragment was cloned in pMa5-8 yielding pJB3. By site-directed mutagenesis, a NcoI site was created at the initiation codon to yield pVE29. A fragment containing the truncated gene fragment of the bt15 gene, with a translational stop codon, was obtained by isolation of BclI-ClaI from POH50 and cloning in PLK91, yielding pHW38. The whole toxin gene fragment was reconstructed under the control of the tac promoter, yielding pVE35, by ligation of a ClaI-PstI fragment from pHW38, a NcoI-ClaI fragment from pVE29 and a NcoI-PstI fragment from pOH48. A truncated bt15 gene fragment with a NcoI site at the initiation codon was obtained from pVE35 as a 1980 NcoI-BaMHI fragment and cloned in pGSJ141, digested with ClaI and BamHI. pGSJ141 has been described in EPA 88402115.5. Ligation of the filled ClaI site to the filled NcoI site yielded a chimeric TR2' - truncated bt15 - 3'g7 construct (pTVE47). As a selectable marker in this plasmid, the bar gene encoding phosphinothricin acetyl transferase and conferring

resistance to PPT was used. A chimeric bar gene containing the bar gene under the control of the 35S promoter and followed by the 3' end of the octopine synthase was introduced in pTVE47. From pDE110, a 35S-bar-3'ocs fragment was obtained as a stul-HindIII fragment and was cloned in pTVE47 digested with PstI and HindIII. This yielded the plasmid pTHW88 (Figure 15) which contains the truncated bt15 gene under the control of the TR2' promoter and the bar gene under the control of the 35S promoter between the T-DNA border repeats. Plasmid pGSH163 is cointegration type Ti-plasmid vector, whereas pTHW88 is a binary type Ti-plasmid vector as described in EPA 0193259.

Both plasmids were mobilized in the A. tumefaciens strain C58C1RiF (pGV2260) according to Deblaere et al. (1988). In the sequential transformation procedure, tomato was transformed according to De Block et al. (1987) with the A. tumefaciens strain C58C1RiF carrying pGS1163 resulting from the cointegration of pGSH163 and pGV2260. Individual transformants were selected for kanamycin resistance, and regenerated plants were characterized for expression of the truncated bt2 gene according to Vaeck et al. (1987). One representative transformant was subsequently retransformed with the A. tumefaciens strain C58C1RiF (pGV2260 and pTHW88), and transformants were selected for PPT resistance. Using this cotransformation procedure, the respective Agrobacteria strains, carrying the cointegrate vector pGS1163 and the binary vector pTHW88, were used for transformation of tomato. Individual plants were selected for resistance to Km and PPT.

Schematically shown in Fig. 15 are:

a) construction of pVE29: bt15 N-terminal gene fragment with NcoI site introduced at ATG initiation codon.

b) construction of pVE35: bt15 C-terminal truncated gene fragment under control of the tac promoter.

c) construction of pTHW88: binary T-DNA vector with a chimeric bt15 gene and a chimeric bar gene within the T-DNA border repeats.

In both cases, co-expression of the two ICP genes in the individual transformants was evaluated by insect toxicity tests as described in EP 0193259 and by biochemical means. Specific RNA probes allowed the quantitive analysis of the transcript levels; monoclonal antibodies cross-reacting with the respective gene products allowed the quantitative analysis of the respective gene products in ELISA tests (EP 0193259); and specific DNA probes allowed the characterization of the genomic integrations of the bt2 and bt15 genes in the transformants. It was found that the transformed tomato plants simultaneously expressed both the bt2 gene (8.1 ng/mg) and the bt15 gene (7.6 ng/mg) as measured by ELISA, which would prevent or delay development of resistance of M. sexta to the insecticidal effects of the Bt2 and Bt15 toxins, being expressed.

These procedures also could be applied when one or both ICP genes are part of a hybrid gene. For example, the same strategy as described above could be followed with the plasmid vectors pGSH152, containing a chimeric truncated bt2-neo hybrid gene under control of the TR2' promoter, and pTHW88 in suitable Agrobacterium strains.

EXAMPLE 10: Separate transfer of two ICP genes to the nuclear genome of separate plants in independent transformation events and subsequent combination in a single plant through crossing.

Tobacco plants have been transformed with either the bt18 gene or the bt15 gene by applying the same cloning strategies as described in EP 0358557 and EP 193259, respectively. For both genes, the plants were transformed with plant expression vectors containing either the truncated bt18 or bt15 gene, which just encode the Bt18 or Bt15 toxin, respectively.

The mortality rate of Spodoptera littoralis larvae feeding on the transformed plants is significantly higher than the mortality rate of larvae fed on untransformed plants.

The bt18-transformed plant, which is homozygous for the bt18 gene, is then crossed with the bt15 -transformed plant, which is homozygous for the bt15 gene. After selfing, a plant homozygous for both genes is obtained.

The resulting tobacco plants, expressing both the bt18 and bt15 genes, delay significantly development of resistance by S. littoralis to either the Bt18 or Bt15 toxin expressed by the plants.

EXAMPLE 11: Transfer of two chimeric ICP genes linked within the same DNA to the genome of plant cells

The strategy used is based on the organization of two independent chimeric ICP genes between the T-DNA border repeats of a single vector. Binding studies indicated that the Bt2 and Bt14 toxins are two non-competitively binding ICPs with insecticidal activity towards Pieris brassicae. For expression in plants, both the bt2 and bt14 genes can be co-expressed to prevent insect resistance development. For the design of a plasmid

vector with each ICP gene under the control of a separate- promoter, two possibilities can be envisaged: 1) three chimeric constructs carrying the truncated bt2 and bt14 genes and a selectable marker, respectively; or 2) a hybrid of a truncated gene fragment (bt2 or bt14) and the neo gene can be used in combination with a truncated bt14 or bt2 gene.

This Example describes the construction of the vector pTHW94 for plant transformations carrying the following chimeric ICP genes between the T-DNA border repeats: a truncated bt2 gene fragment under the control of the TR2' promoter and a hybrid truncated bt14-neo gene under the control of the TR1' promoter. The 3' end of the T-DNA gene 7 and octopine synthase, respectively, provide information for proper 3' end formation. pTHW94 has been deposited at the DSM under accession no. 5514 on August 28, 1989.

Schematically shown in Fig. 16 are the:

a) construction of pHW44: bt14 N-terminal gene fragment with NcoI site introduced at ATG initiation codon.

b) construction of pHW67: reconstruction of the bt14 gene under the control of the tac promoter.

c) construction of pHW71: construction of a hybrid truncated bt14-neo gene under the control of the tac promoter.

d) construction of pTHW94: binary T-DNA vector with chimeric bt14 gene and a chimeric bt2 gene within the T-DNA border repeats.

The pTHW94 vector is mobilized into the Agrobacterium strain C58C1RiF (pMP90) which is used to transform Brassica napus according to the procedure described by De Block et al. (1989). Transformants are selected on Km, and regenerated plants are found to express both ICP gene products in insect toxicity tests and biochemical tests.

EXAMPLE 12: Expression of two ICP genes in a hybrid construct

In order to obtain a combined and simultaneous expression of two ICP genes, truncated gene fragments encoding the toxic parts of two different ICPs can be fused in a proper reading frame and placed, as a hybrid gene, under the control of the same promoter in a chimaeric gene construct. Toxic cores from certain ICPs can be liberated from their protoxins by protease activation at the N- and/or C- terminal end. Thus, hybrid genes can be designed with one or more regions encoding protease cleavage site(s) at the fusion point(s) of two or more ICP genes.

The simultaneous co-expression of the bt2 and bt14 genes is obtained by constructing a hybrid gene composed of a truncated bt14 gene fragment fused to a truncated bt2 gene fragment. Schematically shown in Figure 17 is the construction of such a hybrid bt2-bt14 gene with a C-terminal bt2 gene fragment (bt860) encoding the toxic core of the Bt2 protoxin in frame with a C-terminal truncated bt14 gene fragment encoding the toxic core of the Bt14 protoxin. The BclI site in the bt2 gene, localized downstream of the trypsin cleavage site, is fused in frame with the NcoI site introduced at the N-terminal end of the truncated bt14 gene fragment. To this end, the plasmids pLBKm860 (EP 0193259) and pHW67 are used. pLBKm860 contains a hybrid bt2-neo gene under control of the lambda P_L promoter. The bt2 gene moiety in the hybrid gene is a C-terminal truncated bt2 gene fragment, indicated as bt860 (in Fig. 17) (see also Vaeck et al, 1987). The construction of pHW67 is described in Fig. 16. pHW67 contains a C-terminal truncated bt14 gene fragment (bt14tox) with a NcoI site at the ATG initiation codon, a translation stop codon located at the BCII site of the intact bt14 gene and a BamHI site downstream of the whole gene fragment. To fuse both gene fragments in the proper reading frame, the BclI and NcoI ends of the respective plasmids are treated with Klenow DNA polymerase and S1 nuclease as indicated in Figure 16. The resulting plasmid pJB100 contains the hybrid bt860-bt14tox gene under control of the lambda P_L promoter and directs the expression in E. coli of a fusion protein with the expected mobility on SDS-PAGE.

Crude extracts of the E. coli strain show the toxicity of the fusion protein, expressed by the strain, against P. brassicae. It has also been conf irmed by N-terminal amino acid sequence analyses of the fusion protein produced by the E. coli strain that the N-terminal amino acids from the Bt14 protoxin are processed upon activation. The bt2-bt14 hybrid gene product has thus two potential protease cleavage sites.

Subsequently, this hybrid gene is inserted into a vector for plant transformations and placed under control of a suitable promoter and transferred to the genome of brassica (EP 0193259) where both the bt2 and bt14 genes are expressed in insect toxicity tests.

Table 2

Gene	Bt strain	Host range	amino acids encoded	predicted MW(kDa) of encoded aminoacids	Disclosure of nucleotide sequence
bt3	HD-1 kurstaki	L	1176	133.2	Schnepf et al.,1985
bt2	berliner 1715	L	1155	131	Höfte et al.,1986
bt73	HD-73	L	1178	133.3	Adang et al, 1985
bt14	entomocidus HD-110	L	1207	138	Brizzard and Whiteley, 1988
bt15	entomocidus HD-110	L	1189	134.8	Fig. 14
bt4	HD-68 aizawai	L	1165	132.5	Fig. 13
bt18	darmstadiensis HD-146	L	1171	133	EP appln. 88402241.9
bt13	BtS1,DSM4288 22/10/87	C	644	73.1	EP appln. 88402115.5
bt21	BtPGSI208, DSM 5131, 19/1/89	C	651	74.2	EP appln. 89400428.2
bt22	BtPGSI245, DSM 5132, 19/1/89	C	1138	129	EP appln. 8940028.2
P2	HD-263	L/D	633	70.9	Donovan et al. 1988
Cry B2	HD-1	L	633	70.8	Widner and Whiteley, 1989

REFERENCES

- Adang H., Staver M., Rocheleau T., Leighton J., Barker R. and Thompson D. (1985), Gene 36, 289-300.
- Angenon et al (1989), Molecular and Cellular Biology 9, 5676-5684.
- Barton K., Whiteley H. and Yang N.-S. (1987), Plant Physiol. 85, 1103-1109.
- Bernard H., Remaut E., Hersfield M., Das H., Helinski D., Yanofski C. and Franklin N. (1979), Gene 5, 59-76.
- Bell R. and Joachim F. (1976), Ann. Entomol. Soc. Am. 69, 365-373.
- Botterman J. and Zabeau M. (1987), DNA 6, 583-591.
- Bradford M. (1976), Anal. Biochem. 72, 248-254.
- Brattsten L., Holyoke C., Leeper J. and Raffa K. (1986), Science 231, 1255-1260.
- Brizzard B. and Whiteley H. (1988), Nucleic Acids Research 16, 4168-4169.
- Deblaere R., Reynaerts A., Höfte H., Hernalsteens J-P, Leemans J. and Van Montagu M. (1988), Methods in Enzymol. 153, 277-292.
- De Block M., Botterman J., Vandewiele M., Dockx J., Thoen, Gosselé V., Rao Mowa, Thompson C., Van Montagu M. and Leemans J. (1987), EMBO J. 6, 2513-2518.
- De Block et al (1989), Plant Physiology 91, 694-701.
- De Boer H., Comstock L. and Vasser M. (1983), Proc. Natl. Acad. Sci. USA 80, 21-25.
- de Framond A., Back E., Chilton W., Kayes L. and Chilton M-D (1986), Mol. Gen. Genet. 202, 125-131.
- De Greve et al (1982), J. Mol. Appl. Genet. 1 (6), 499-511.
- De La Pena and Schell (1986), Nature 325, 274-276.
- Delauney A., Tabaeizadeh Z. and Verma D. (1988), Proc. Natl. Acad. Sci. USA 85, 4300-4304.
- Depicker A., Herman L., Jacobs A.,Schell J. and Van Montagu M. (1985), Mol. Gen. Genet. 201, 477-484.
- Donovan W., Dankoscik C. and Gilbert W. (1988), J. Bacteriol. 170, 4732-4738.
- Dulmage H.T and cooperators (1981), In : Microbial control of pests and plant diseases 1970-1980 (Ed. N.D. Burges), Academic Press, 193-222.
- Finney D. (1962), Probit Analysis (University Press, Cambridge), pp. 50-80.
- Fischhoff D., Bowdish K., Perlak F., Marrone P., McCormick S., Niedermeyer J., Dean D., Kuzano-Kretzmer K., Mayer E., Rochester D., Rogers S. and Fraley R. (1987), Bio/Technology 5, 807-812.
- Franck, Guilley, Jonard, Richards and Hirth (1980), Cell 21, 285-294.
- French B., Maul H. and Maul G. (1986), Anal. Biochem. 156, 417-423.
- Fuller F. (1982), Gene 19, 43-54.
- Gardner, Howarth, Hahn, Brown-Luedi, Shepard and Messing, Nucl. Acids Res. 9, 2871-2887.
- Goldberg L. and Margalit J. (1977), Mosq. News 37, 355-358.
- Goldman I., Arnold J. and Carlton 9. (1986), J. Invert. Pathol. 47, 317-324.
- Gould F. (1988), Bioscience 38, 26-33.
- Haider M., Knowles B. and Ellar D. (1986), Eur. J. Biochem. 156, 531-540.
- Herrera-Estrella (1983) Nature 303, 209-213.
- Hofmann C., Lüthy P., Hutter R. and Pliska V. (1988a), Eur. J. Biochem. 173, 85-91.
- Hofmann C., Vanderbruggen H., Höfte H., Van Rie J., Jansens S. and Van Mellaert H. (1988b), Proc. Natl. Acad. Sci. USA 85, 7844-7848.
- Höfte H., Van Rie J., Jansens S., Van Houtven A., Verbruggen H. and Vaeck M. (1988), Appl. Environ. Microbiol. 54, 2010-2017.
- Höfte H., De Greve H., Seurinck J., Jansens S., Mahillon J., Ampe C., Vanderkerkhove J., Vanderbruggen H., Van Montagu M., Zabeau M. and Vaeck M. (1987), Eur. J. Biochem. 161, 273-280.
- Höfte H. and Whiteley H.R. (1989), Microbiological Reviews 53, 242-255.
- Hsiung H. and Becker G. (1988), Biotech. and Genetic Engin. Rev. 6, 43-65.
- Hull and Howell (1987), Virology 86, 482-493.
- Hunter W. and Greenwood F. (1962), Nature 194, 495-496.
- Kozak M. (1987), Mol. Cell. Biol. 7, 3438-3445.
- Krebbers E., Herdies L., De Clercq A., Seurinck J., Leemans J., Van Damme J., Segura M.,Gheysen G., Van Montagu M. and Vandekerckhove J. (1988), Plant Physiol. 87, 859-866.
- Knowles B. and Ellar D. (1986), J. Cell. Sci 83, 89-101.
- Krieg A., Huger A., Langenbruch G. and Schnetter W. (1983), Z. Ang. Ent. 96, 500-508.
- Krieg A. and Langenbruch G. (1981), In : Microbial control of pests and plant diseases 1970-1980 (Ed. H.D. Burges), Academic Press, 837-986.
- Kirsch K. and Schmutterer H. (1988), J. Appl. Ent. 105, 249-255.

- Kronstad J., Schnepf H. and Whiteley H. (1983), J. Bacteriol. 154, 419-428.
- Mahillon J. and Delcour J. (1984), J. Microbiol. Methods 3, 69-73.
- Maxam A. and Gilbert in. (1980), Methods in Enzymol. 65, 499-560.
- McGaughey W. (1985), Science 229, 193-195.
- McGaughey W. and Beeman R. (1988), J. Econ. Entomol. 81, 28-33.
- Munson P. and Rodbard D. (1980), Anal. Biochem. 107, 220-239.
- Pazkowski and cooperators (1984), J 3, 2717-2722.
- Peleman J., Boerjan W., Engler G., Seurinck J., Botterman J., Alliote T., Van Montagu M. and Inzé D. (1989), The Plant Cell 1, 81-93.
- Remaut E., Stanssen P. and Fiers W. (1981), Gene 15, 81-93.
- Rocha-Sosa et al (1989) EMBO J. 8, 23-29.
- Sandler S., Stayton M., Townsend J., Ralstan M., Bedbrook J. and Dunsmuir P. (1988), Plant Mol. Biol. 11, 301-310.
- Scatchard G. (1949), Ann. N.Y. Acad. Sci. 51, 660-672.
- Schocher R., Shillito R., Saul M.,Pazkowski J. and Potrykus I. (1986) Bio/technology 4, 1093-1096.
- Shields (1987), Nature 328, 12-13.
- Schnepf H., Wong H. and Whiteley H. (1985), J. Biol. Chem. 260, 6264-6272.
- Stanssens P., Remaut E. and Fiers W. (1985), Gene 36, 211-223.
- Stanssens P., McKeown Y., Friedrich K. and Fritz H. (1987) : "Oligo-nucleotide directed construction of mutations by the gapped duplex DNA method using the pMa/c plasmid vectors", published in the Collection of Experimental Procedures distributed at the EMBO course entitled "Directed mutagenesis and protein engineering" in July 1987 at the Max Planck Institut für Biochemie, Martinsried, FRG.
- Stone T., Sims S. and Marrone P. (1989), J. Invert. Pathol. 53, 228-234.
- Vaeck M., Reynaerts A., Höfte H., Jansens S., De Beukeleer M., Dean C. Zabeau M., Van Montagu M. and Leemans J. (1987), Nature 327, 33-37.
- Voller, Bidwell and Barlett (1976), In: Manual of Clinical Immunology (Eds. Rose and Friedman), pp. 506-512, American-Society of Microbiology, Washington
- Velten J., Velten L., Hain R. and Schell J. (1984), EMBO J. 3, 2723-2730.
- Velten J. and Schell J. (1985), Nucl. Acids Res. 13, 6981-6998.
- Widner W. and Whiteley H. (1989), J. Bacteriol. 171, 965-974.
- Wolfersberger M., Lüthy P., Maurer A., Parenti P., Sacchi V., Giordana B. and Hanozet G. (1987), Comp. Biochem. Physiol. 86, 301-308.
- Yanish-Perron C., Veiera J. and Messing J. (1985), Gene 33, 103-119.

Claims

1. Cells of a plant, characterized by: at least two B. thuringiensis Insecticidal Crystal Protein genes stably inserted into the genome of said plant; said genes being under the control of the same or distinct promoter and each of said genes encoding a different non-competitively binding Insecticidal Crystal Protein for the same insect species; whereby at least two different Insecticidal Crystal Proteins can be produced in cells of said plant.

2. Cells of Claim 1 wherein at least one marker gene, encoding a protein or polypeptide which renders said cells easily distinguishable from cells which do not contain said protein or polypeptide, is in the same genetic locus as at least one of said Insecticidal Crystal Protein genes.

3. Cells of Claim 1 or 2, wherein each of said Insecticidal Crystal Protein genes is under the control of a separate promoter capable of directing gene expression in said cells and is provided with a separate signal for 3' end formation and within a same transcriptional unit.

4. Cells of Claim 2 or 3, in which said marker gene is under the control of a separate promoter capable of directing gene expression in said plant cells and is provided with a signal for 3' end formation within a same transcriptional unit.

5. Cells of Claim 1 or 2, wherein said Insecticidal Crystal Protein genes are within a same transcriptional unit and under the control of a single promoter.

6. Cells of Claim 5, wherein said marker gene is fused with at least one of said Insecticidal Crystal Protein genes and is within said same transcriptional unit and under the control of said promoter.

7. Cells of Claim 5 or 6, wherein a DNA fragment, encoding a protease-sensitive or - cleavable amino acid sequence, is in said same transcriptional unit as said Insecticidal Crystal Protein genes and intercalated in frame between said Insecticidal Crystal Protein genes.

8. Cells of Claim 5 or 6, wherein said Insecticidal Crystal Protein genes are combined in a dicistronic unit comprising an intergenic DNA sequence which allows reinitiation of translation and is in said same transcriptional unit as said Insecticidal Crystal Protein genes and intercalated between said Insecticidal Crystal Protein genes.

9. Cells of any one of Claims 1 to 8, wherein said Insecticidal Crystal Protein genes are encoding insecticidal proteins having activity against Lepidoptera species and are particularly the following genes: bt2 and/or bt73 and/or bt4 and/or bt14 and/or bt15 and/or bt18.

10. Cells of any one of Claims 1 to 8, wherein said Insecticidal Crystal Protein genes are genes encoding insecticidal proteins having activity against a Coleoptera species and are particularly the following genes: bt13 and/or bt21 and/or bt22.

11. Cells of any one of Claims 2 to 10 wherein said marker gene is: a herbicide resistance gene, particularly a sfr or sfrv gene; a gene encoding a modified target enzyme for a herbicide having a lower affinity for the herbicide, particularly a modified 5-EPSP as a target for glyphosate or a modified glutamine synthetase as a target for a GS inhibitor; or an antibiotic resistance gene, particularly NPTII.

12. Cells of any one of Claims 1 to 11, wherein any of said same or distinct promoters of said Insecticidal Crystal Proteins are selected from the group of: a constitutive promoter, particularly a 35S promoter or a 35S3 promoter; a PNOS promoter; a POCS promoter; a wound-inducible promoter, particularly a TR1' or TR2' promoter; a promoter which directs gene expression selectively in plant tissue having photosynthetic activity, particularly a SSU promoter; or a tissue-specific or an organ specific promoter, particularly a tuber-specific promoter, a stem-specific promoter or a seed-specific promoter or an inducible promoter, particularly a promoter induced by chemical factors or temperature or combinations thereof.

13. A vector suitable for transforming cells of a plant, particularly a plant capable of being infected with Agrobacterium, comprising said Insecticidal Crystal Protein genes of any one of Claims 1 to 12.

14. A process for producing a plant having improved insect resistance and having said Insecticidal Crystal Protein gene combinations of any one of Claims 1 to 12 stably integrated into the nuclear genome of its cells, characterized by the non-biological steps of transforming a plant cell by introducing the Insecticidal Crystal Protein gene combinations of any one of Claims 1 to 12 into the nuclear genome of said cell and regenerating said plant and reproduction material from said cell.

15. A plant cell culture, consisting of the plant cells of any one of Claims 1 to 12.

16. A plant, consisting of the plant cells of any one of Claims 1 to 12.

17. Brassica, tomato, potato, tobacco, cotton or lettuce consisting of the plant cells of any one of Claims 1 to 12, wherein said Insecticidal Crystal Protein genes comprise one of the following pairs of genes: bt2 and bt18 or bt73 and bt15 or bt2 and bt18 or bt2 and bt14 or bt2 and bt4 or bt15 and bt18 or bt14 and bt15 or bt4 and bt15 or bt13 and bt21 or bt21 and bt22 or bt13 and bt22.

18. A method for rendering a plant resistant to an insect species by transforming the plant with said Insecticidal Crystal Protein genes of any one of Claims 1-12.

19. A plant characterized by: at least two B. thuringiensis Insecticidal Crystal Protein genes stably inserted into the genome of said plant; said genes being under the control of the same or distinct promoter and each of said genes encoding a different non-competitively binding Insecticidal Crystal Protein for the same insect species; whereby at least two different Insecticidal Crystal Proteins can be produced in cells of said plant.

20. Cells of a plant according to Claim 1 wherein said B. thuringiensis Insecticidal Crystal Protein genes have naturally occurring or synthetic nucleotide sequences.

Patentansprüche

1. Pflanzenzellen, dadurch gekennzeichnet, daß wenigstens zwei B. thuringiensis insecticidal crystal protein - Gene stabil in das Genom dieser Pflanze eingesetzt sind, diese Gene der Kontrolle desselben oder eines jeweils bestimmten Promoters unterliegen und jedes dieser Gene ein anderes, ohne wechselseitige Beeinflussung eingebundenes insecticidal crystal protein verschlüsselt, wobei die wenigstens zwei Insecticidal crystal proteine in Zellen dieser Pflanzen erzeugt werden können.

2. Zellen nach Anspruch 1, wobei wenigstens ein Markierungsgen, das ein Protein oder Polypeptid verschlüsselt, das diese Zellen leicht von den Zellen unterscheiden läßt, die dieses Protein oder Polypeptid nicht enthalten, sich an derselben genetischen Stelle befindet wie wenigstens eines dieser insecticidal crystal protein - Gene.

3. Zellen nach Anspruch 1 oder 2, wobei jedes dieser insecticidal crystal protein - Gene der Kontrolle eines anderen Promoters unterliegt, der die Umsetzung der Gene in diesen Zellen steuern kann und mit einem getrennten Signal für 3' - Endbildung innerhalb derselben Transcriptase-Einheit versehen ist.

4. Zellen nach Anspruch 2 oder 3, wobei jedes der Markierungsgene der Kontrolle eines anderen Promoters unterliegt, der die Umsetzung der Gene in diesen Zellen steuern kann und mit einem getrennten Signal für 3' - Endbildung innerhalb derselben Transcriptase-Einheit versehen ist.

5. Zellen nach Anspruch 1 oder 2, wobei diese insecticidal crystal protein sich in derselben Transcriptase-Einheit befinden und einem Promoter unterliegen.

6. Zellen nach Anspruch 5,wobei das Markierungsgen mit wenigstens einem der insecticidal crystal protein -Gene verbunden ist, sich in derselben Transcriptase-einheit befindet und der Kontrolle desselben Promoters unterliegt.

7. Zellen nach Anspruch 5 oder 6, wobei ein DNA-Bruckstück, das eine protease-empfindliche oder protease-gebundene Aminosäuresequenz verschlüsselt, sich in derselben Transcriptase-Einheit wie die insecticidal crystal protein - Gene befindet und in den Rahmen zwischen den insecti-cidal crystal protein - Genen eingeschoben ist.

8. Zellen nach Anspruch 5 oder 6, wobei diese Insecticidal crystal protein - Gene in einer dicistronischer Einheit zusammengefaßt sind, die eine zwischengenetische DNA-Sequenz umfaßt, die einen erneuten Beginn der Übersetzung erlaubt und sich in derselben Transcriptase-Einheit wie die insecticidal crystal protein - Gene befindet und zwischen diese insecticidal crystal protein - Gene eingeschoben ist.

9. Zellen nach einem der Ansprüche 1 - 8, wobei die insecticidal crystal protein - Gene insecticidal Proteine verschlüsseln, die Aktivität gegen Lepidoptera-Spezien entfalten und besonders die folgenden Gene sind: bt2 und/oder bt73 und/oder bt4 und/oder bt14 und/oder bt15 und/oder bt18 .

10. Zellen nach einem der Ansprüche 1 - 8, wobei die insecticidal crystal protein - Gene insecticidal Proteine verschlüsseln, die Aktivität gegen eine Coleoptera-Spezies entfalten und besonders die folgenden Gene sind: bt13 und/oder bt21 und/oder bt22

11. Zellen nach einem der Ansprüche 2 - 10, wobei das Markierungsgen ein herbizidresistentes Gen ist, insbesondere ein sfr oder sfrv Gen, oder ein Gen ist, das ein verändertes Zielenzym für ein Herbizid mit geringerer Empfindlichkeit gegenüber diesem Herbizid verschlüsselt, insbesondere ein verändertes 5-EPSP als Ziel für Glyphosat oder eine veränderte Glutamin-Synthetase als Ziel für einen GS-Hemmer, oder ein gegen Antibiotika resistentes Gen ist, insbesondere NPTII.

12. Zellen nach einem der Ansprüche 1 - 11, wobei jeder beliebige dieser gleichen oder jeweils bestimmten Promoter dieser insecticidal crystal proteine aus einer Gruppe ausgewählt ist, die sich zusammensetzt aus einem angeborenen Promoter, insbesondere einem 35S oder 35S3 Promoter, einem PNOS Promoter,

einem durch Verletzung einführbaren Promoter, insbesondere einem TR1' oder TR2' Promoter, einem Promoter, der die Entfaltung der Gene gesteuert in Pflanzengewebe mit photosynthetischer Aktivität richtet, insbesondere einem SSU Promoter, oder einem gewebe- oder organspezifischen Promoter, insbesondere einem knollenspezifischen Promoter, einem stengel- oder samenspezifischen Promoter, oder einem einführbaren Promoter, insbesondere einem Promoter, der durch chemische Faktoren oder Temperatur oder Kombinationen davon einführbar ist.

13. Ein Bakterienüberträger geeignet zur Veränderung von Pflanzenzellen, insbesondere einer Pflanze, die mit Agrobakterium infiziert werden kann, der die insecticidal crystal protein - Gene nach einem der Ansprüche 1 - 12 enthält.

14. Verfahren zur Erzeugung einer Pflanze, die eine erhöhte Widerstandsfähigkeit gegen Insekten besitzt und stabil in das Kerngenom ihrer Zellen eingesetzte insecti-cidal crystal protein - Genkombinationen nach einem der Ansprüche 1 - 12 aufweist, gekennzeichnet durch die nichtbiologischen Schritte der Veränderung einer Pflanzenzelle durch Einführen der insecticidal crystal protein -Genkombination nach einem der Ansprüche 1 - 12 in das Kerngenom dieser Zelle und das Wiederherstellen dieser Pflanze und des Vermehrungsmaterials ausgehend von dieser Zelle.

15. Eine Pflanzenzellenkultur, bestehend aus Pflanzenzellen nach einem der Ansprüche 1 - 12.

16. Eine Pflanze, bestehend aus Pflanzenzellen nach einem der Ansprüche 1 - 12.

17. Kohl, Tomaten, Kartoffeln, Tabakpflanzen, Wollpflanzen oder Salat, bestehend aus den Pflanzenzellen nach einem der Ansprüche 1 - 12, wobei die insecticidal crystal protein - Gene eines der folgenden Genpaare umfassen: bt2 und bt18 oder bt73 und bt15 oder bt2 und bt18 oder bt2 und bt14 oder bt2 und bt4 oder bt15 und bt18 oder bt14 und bt15 oder bt4 und bt15 oder bt13 und bt21 oder bt21 und bt22 oder bt13 und bt22.

18. Verfahren zur Resistenzerzeugung einer Pflanze gegen eine Insektenspezies durch Veränderung der Pflanze mit den insecticidal crystal protein - Genen nach einem der Ansprüche 1 - 12.

19. Pflanze, gekennzeichnet durch wenigstens zwei stabil in das Genom dieser Pflanze eingefügte B. thuringiensis insecticidal crystal protein - Gene, wobei diese Gene der Kontrolle desselben oder eines jeweils bestimmten Promoters unterliegen und jedes dieser Gene ein anderes, ohne Beeinflussung eingebundes insecticidal crystal protein für dieselbe Insektenspezies verschlüsselt, wobei wenigstens zwei verschiedene insecticidal crystal proteine in den Zellen dieser Pflanze erzeugt werden können.

20. Pflanzenzellen nach Anspruch 1, wobei die B. thuringiensis insecticidal crystal protein - Gene natürlich vorkommende oder synthetische Kernfolgen aufweisen.

Revendications

1. Cellules d'une plante, caractérisées par au moins deux gènes de protéine cristalline insecticide de B. thuringiensis insérés de façon stable dans le génome de cette plante; ces gènes étant sous le contrôle du même promoteur ou de promoteurs distincts et chacun de ces gènes codant pour une protéine cristalline insecticide différente se liant de façon non compétitive pour la même espèce d'insecte; de telle sorte qu'au moins deux protéines cristallines insecticides différentes peuvent être produites dans des cellules de cette plante.

2. Cellules suivant la revendication 1, dans lesquelles au moins un gène marqueur, codant pour une protéine ou un polypeptide permettant à ces cellules d'être facilement distinguées d'autres cellules qui ne contiennent pas cette protéine ou ce polypeptide, est dans le même locus génétique qu'au moins l'un de ces gènes de protéine cristalline insecticide.

3. Cellules suivant les revendications 1 ou 2, dans lesquelles chacun de ces gènes de protéine cristalline insecticide est sous le contrôle d'un promoteur séparé capable de diriger l'expression du gène dans ces cellules et est pourvu d'un signal séparé pour la formation de l'extrémité 3' et dans une même unité transcriptionnelle.

4. Cellules suivant les revendications 2 ou 3, dans lesquelles ce gène marqueur est sous le contrôle d'un promoteur séparé capable de diriger l'expression du gène dans ces cellules végétales et est pourvu d'un signal pour la formation de l'extrémité 3' et dans une même unité transcriptionnelle.

5. Cellules suivant les revendications 1 ou 2, dans lesquelles ces gènes de protéine cristalline insecticide sont dans une même unité transcriptionnelle et sous le contrôle d'un promoteur unique.

6. Cellules suivant la revendication 5, dans lesquelles ce gène marqueur est fusionné à l'un au moins de ces gènes de protéine cristalline insecticide et est dans cette même unité transcriptionnelle et sous le contrôle de ce promoteur unique.

7. Cellules suivant les revendications 5 ou 6, dans lesquelles un fragment d'ADN, codant pour une séquence d'acides aminés pouvant être coupée par une protéase ou sensible à une protéase, est dans la même unité transcriptionnelle que ces gènes de protéine cristalline cristalline et est intercalé dans le cadre entre ces gènes de protéine cristalline insecticide.

8. Cellules suivant les revendications 5 ou 6, dans lesquelles ces gènes de protéine cristalline insecticide sont combinés dans une unité dicistronique comprenant une séquence d'ADN intergénique qui permet une réinitiation de la traduction et est dans la même unité transcriptionnelle que ces gènes de protéine cristalline cristalline et intercalée entre ces gènes de protéine cristalline insecticide.

9. Cellules suivant l'une quelconque des revendications 1 à 8, dans lesquelles ces gènes de protéine cristalline cristalline codent pour des protéines insecticides ayant une activité contre des espèces de Lepidoptera et sont en particulier les gènes suivants : bt2 et/ou bt73 et/ou bt4 et/ou bt14 et/ou bt15 et/ou bt18.

10. Cellules suivant l'une quelconque des revendications 1 à 8, dans lesquelles ces gènes de protéine cristalline cristalline sont des gènes codant pour des protéines insecticides ayant une activité contre une espèce de Coleoptera et sont en particulier les gènes suivants : bt13 et/ou bt21 et/ou bt22.

11. Cellules suivant l'une quelconque des revendications 2 à 10, dans lesquelles ce gène marqueur est : un gène de résistance à un herbicide, en particulier un gène sfr ou sfrv; un gène codant pour une enzyme cible modifiée pour un herbicide ayant une affinité inférieure pour l'herbicide, en particulier un 5-EPSP modifié comme cible pour un glyphosate ou une glutamine synthétase modifiée comme cible pour un inhibiteur de GS; ou un gène de résistance à un antibiotique, en particulier NPTII.

12. Cellules suivant l'une quelconque des revendications 1 à 11, dans lesquelles l'un quelconque de ces promoteurs identiques ou distincts de ces protéines cristallines insecticides est sélectionné parmi le groupe comprenant : un promoteur constitutif, en particulier un promoteur 35S ou un promoteur 35S3; un promoteur PNOS, un promoteur POCS; un promoteur pouvant être induit par une plaie, en particulier un promoteur TR1' ou TR2'; un promoteur qui dirige l'expression génique sélectivement dans un tissu végétal ayant une activité photosynthétique, particulièrement un promoteur SSU; ou un promoteur spécifique d'un tissu ou spécifique d'un organe, en particulier un promoteur spécifique d'une tubercule, un promoteur spécifique d'une tige, un promoteur spécifique d'une graine ou un promoteur inductible, en particulier un promoteur induit par des facteurs chimiques ou la température ou leurs combinaisons.

13. Vecteur convenable pour transformer des cellules d'une plante, en particulier d'une plante pouvant être infectée avec Agrobacterium, comprenant ces gènes de protéine cristalline insecticide de l'une quelconque des revendications 1 à 12.

14. Procédé pour produire une plante ayant une résistance aux insectes améliorée et ayant ces combinaisons de gènes de protéine cristalline insecticide de l'une quelconque des revendications 1 à 12 intégrées de façon stable dans le génome nucléaire de ses cellules, caractérisé par les étapes non biologiques de transformation d'une cellule végétale par introduction des combinaisons de gènes de protéine cristalline insecticide de l'une quelconque des revendications 1 à 12 dans le génome nucléaire de cette cellule et de régénération de cette plante et du matériel de reproduction à partir de cette cellule.

15. Culture de cellules végétales, consistant en cellules végétales de l'une quelconque des revendications 1 à 12.

16. Plante, consistant en cellules végétales de l'une quelconque des revendications 1 à 12.

17. Chou, tomate, pomme de terre, tabac, coton ou laitue, consistant en cellules végétales de l'une quelconque des revendications 1 à 12, dans lesquels ces gènes de protéine cristalline insecticide comprennent l'une des paires de gènes suivantes : bt2 et bt18, ou bt73 et bt15, ou bt2 et bt18, ou bt2 et bt14, ou bt2 et bt4 ou bt15 et bt18, ou bt14 et bt15, ou bt4 et bt15 ou bt13 et bt21, ou bt21 et bt22, ou bt13 et bt22.

18. Méthode pour rendre une plante résistante à une espèce d'insecte par transformation de la plante avec ces gènes de protéine cristalline insecticide de l'une quelconque des revendications 1 à 12.

19. Plante caractérisée par au moins deux gènes de protéine cristalline insecticide de B. thuringiensis insérés de façon stable dans le génome de cette plante; ces gènes étant sous le contrôle du même promoteur ou d'un promoteur distinct et chacun de ces gènes codant pour une protéine cristalline insecticide différente se liant de façon non compétitive pour la même espèce d'insecte; de telle sorte qu'au moins deux protéines cristallines insecticides différentes peuvent être produites dans des cellules de cette plante.

20. Cellules d'une plante suivant la revendication 1, dans lesquelles ces gènes de protéine cristalline insecticide de B. thuringiensis ont des séquences de nucléotides d'origine naturelle ou synthétique.

FIGURE 1

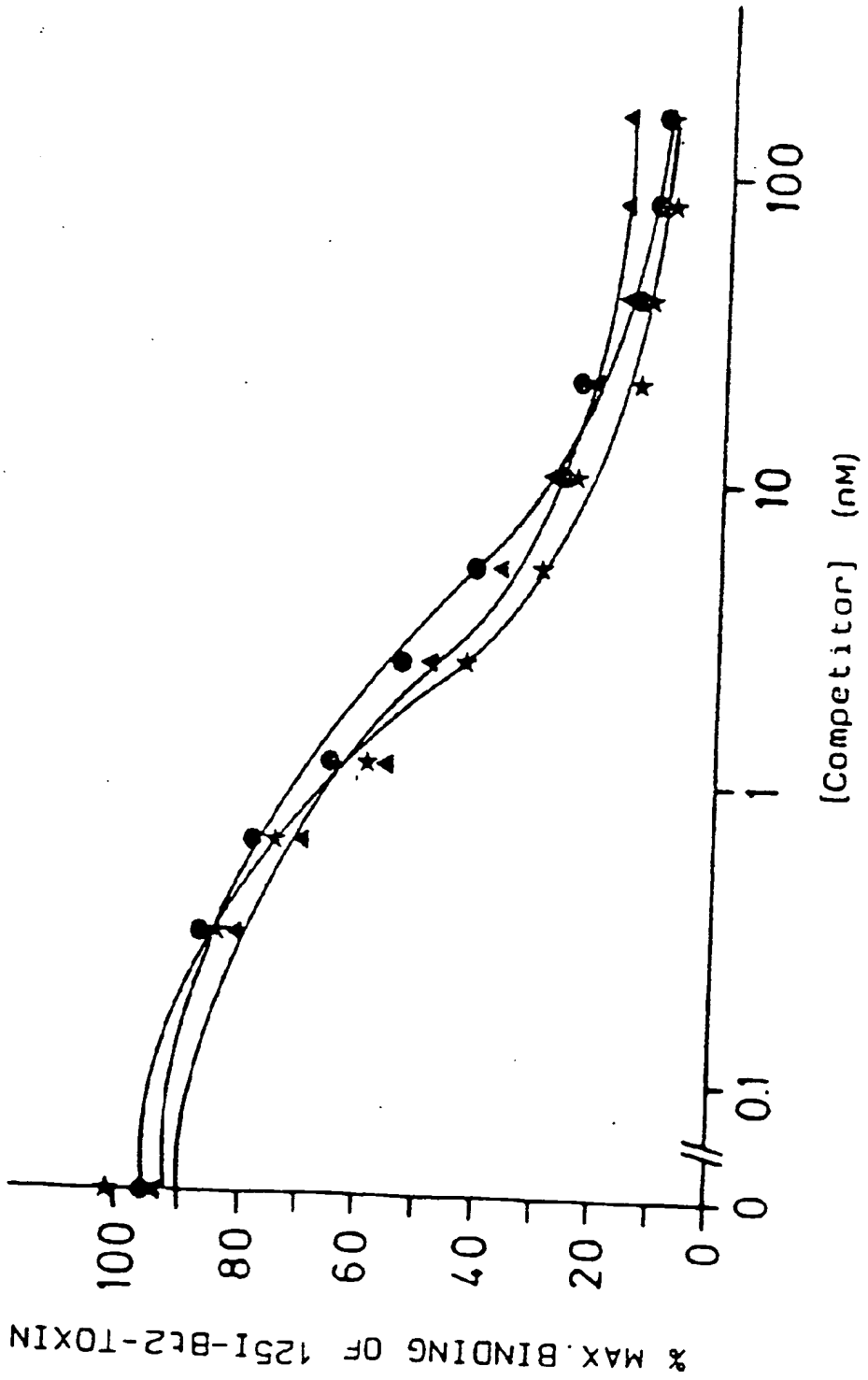

% MAX. BINDING OF 125I-Bt2-TOXIN
100
80
60
40
20
0
0
0.1
1
10
100
[Competitor] (nM)

FIGURE 2

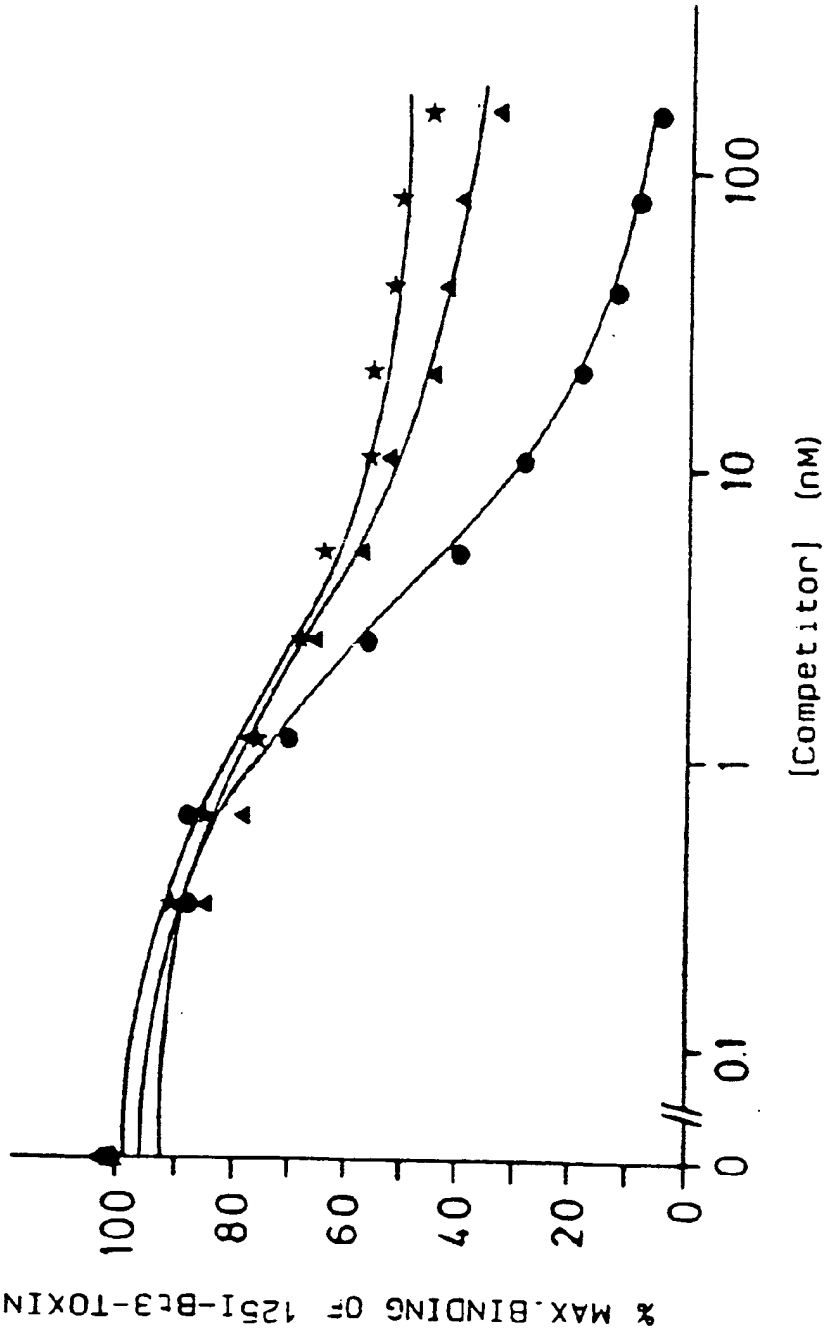

% MAX. BINDING OF 125I-Bt3-TOXIN
100
80
60
40
20
0
0
0.1
1
10
100
[Competitor] (nM)

FIGURE 3

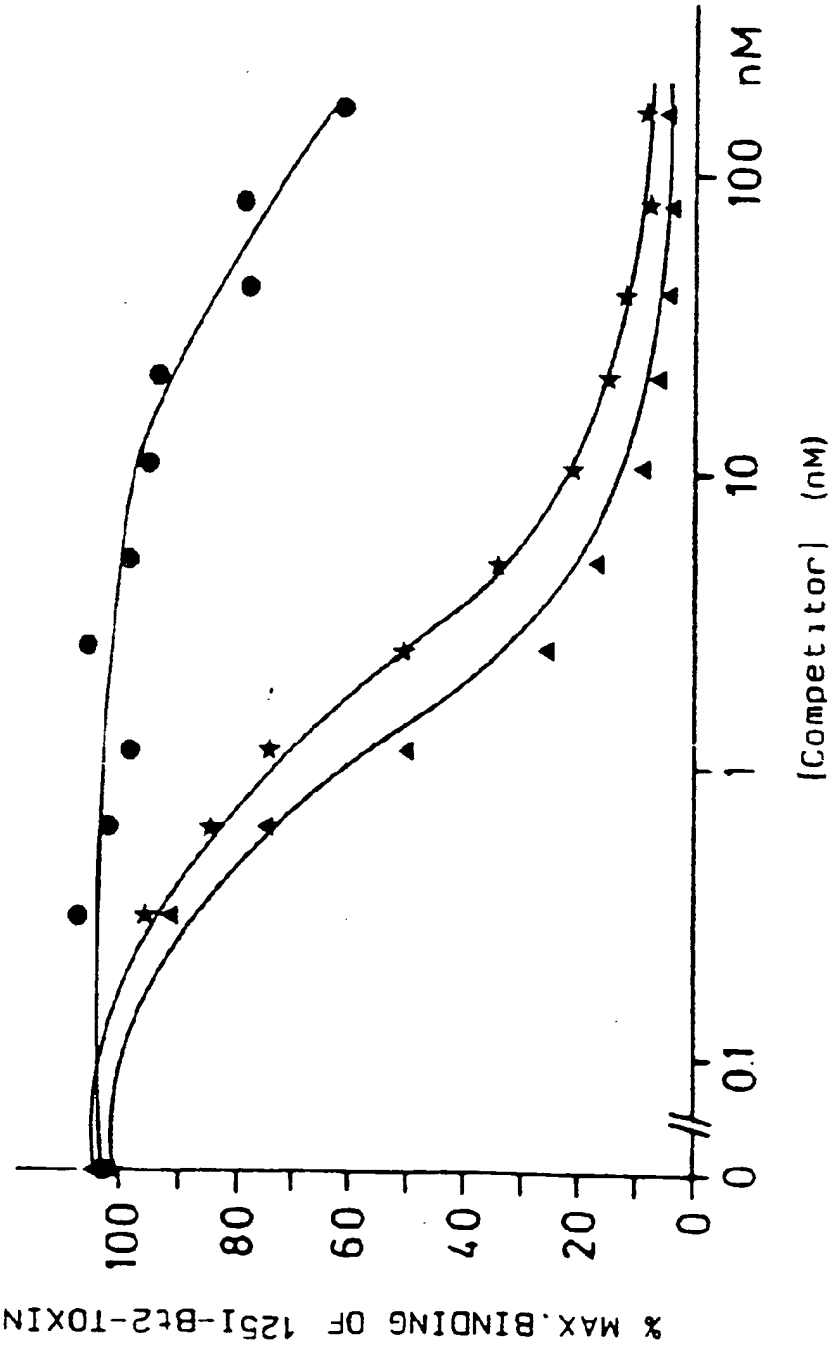

% MAX. BINDING OF 125I-Bt2-TOXIN
100
80
60
40
20
0
0
0.1
1
10
100 nM
[Competitor] (nM)

FIGURE 4

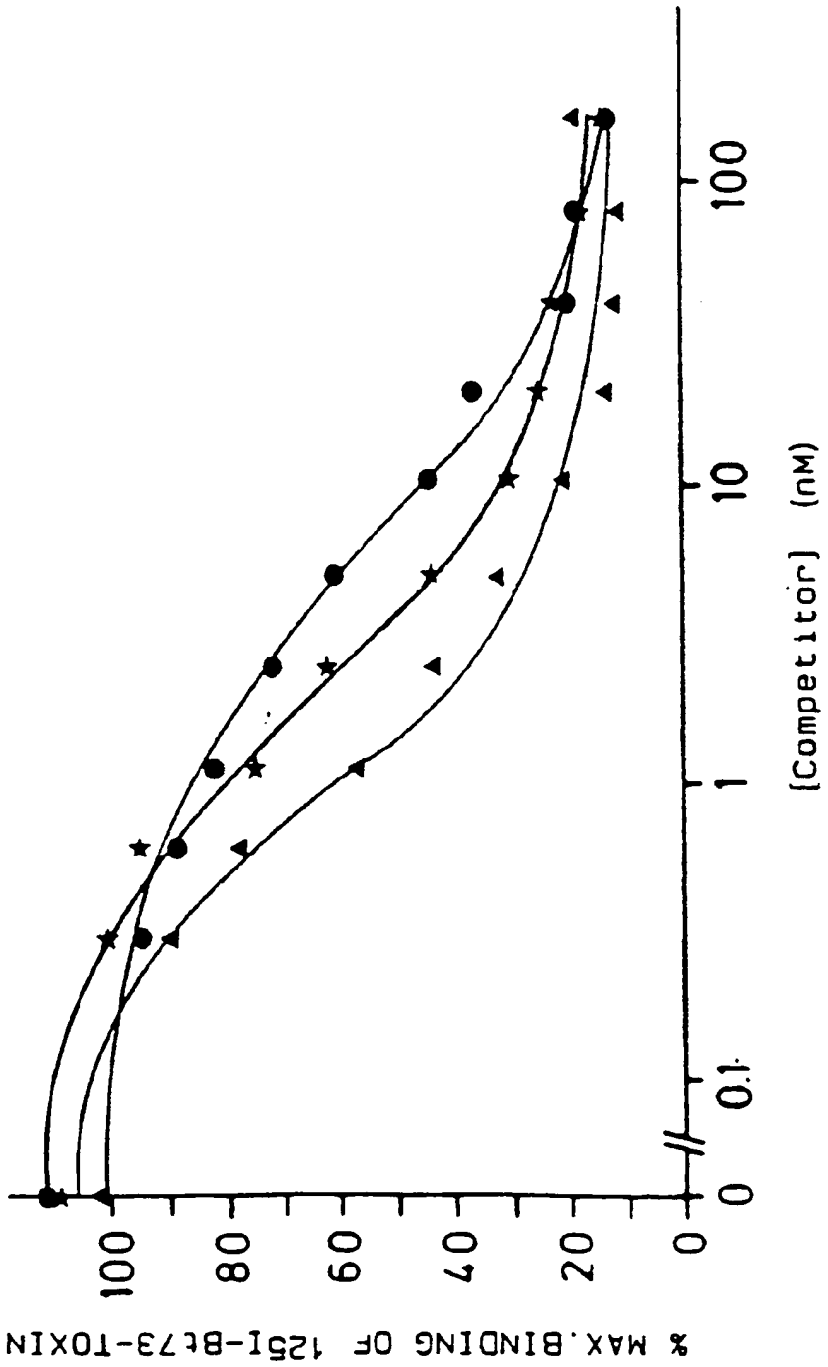

% MAX. BINDING OF 125I-Bt73-TOXIN
100
80
60
40
20
0
0
0.1
1
10
100
[Competitor] (nM)

FIGURE 5

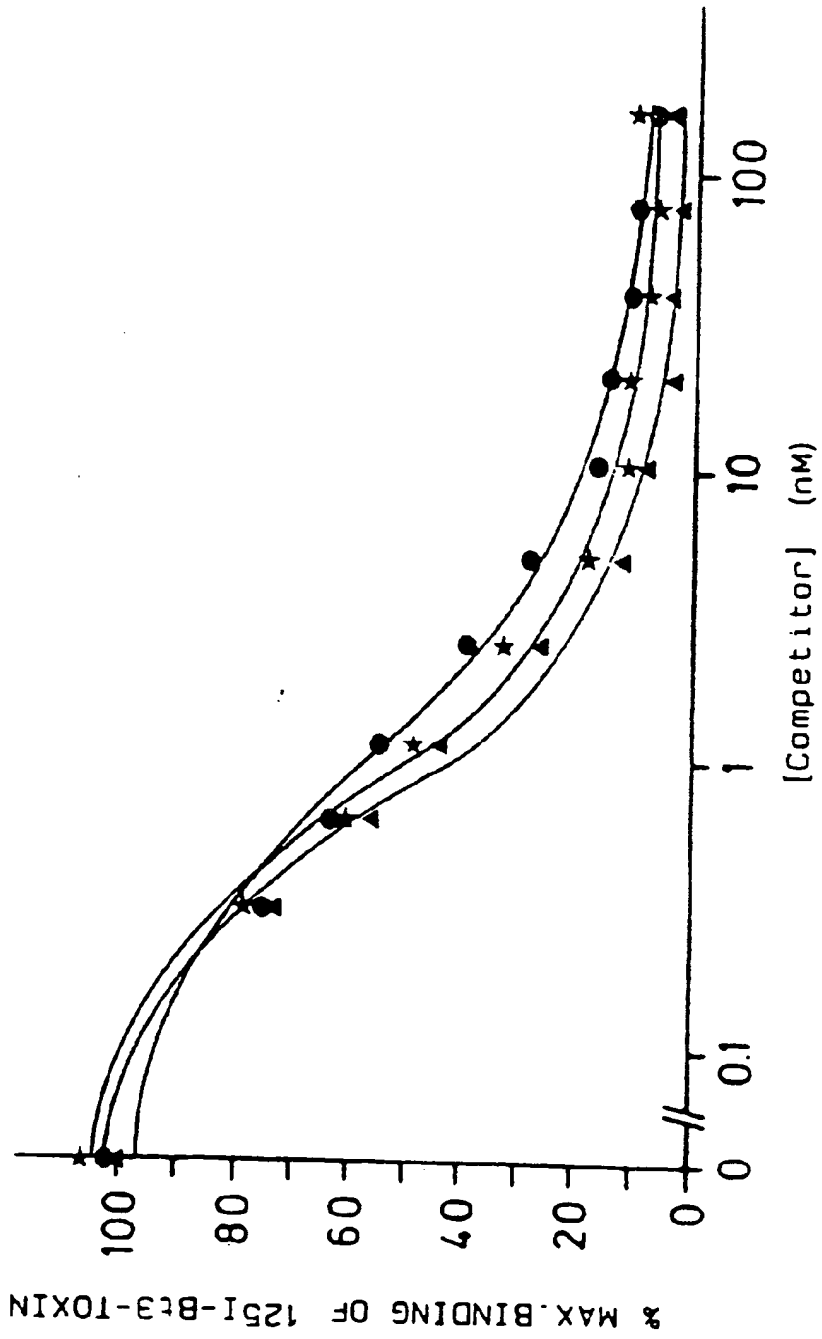

% MAX. BINDING OF 125I-Btg-TOXIN
100
80
60
40
20
0
0
0.1
1
10
100
[Competitor] (nM)

FIGURE 6

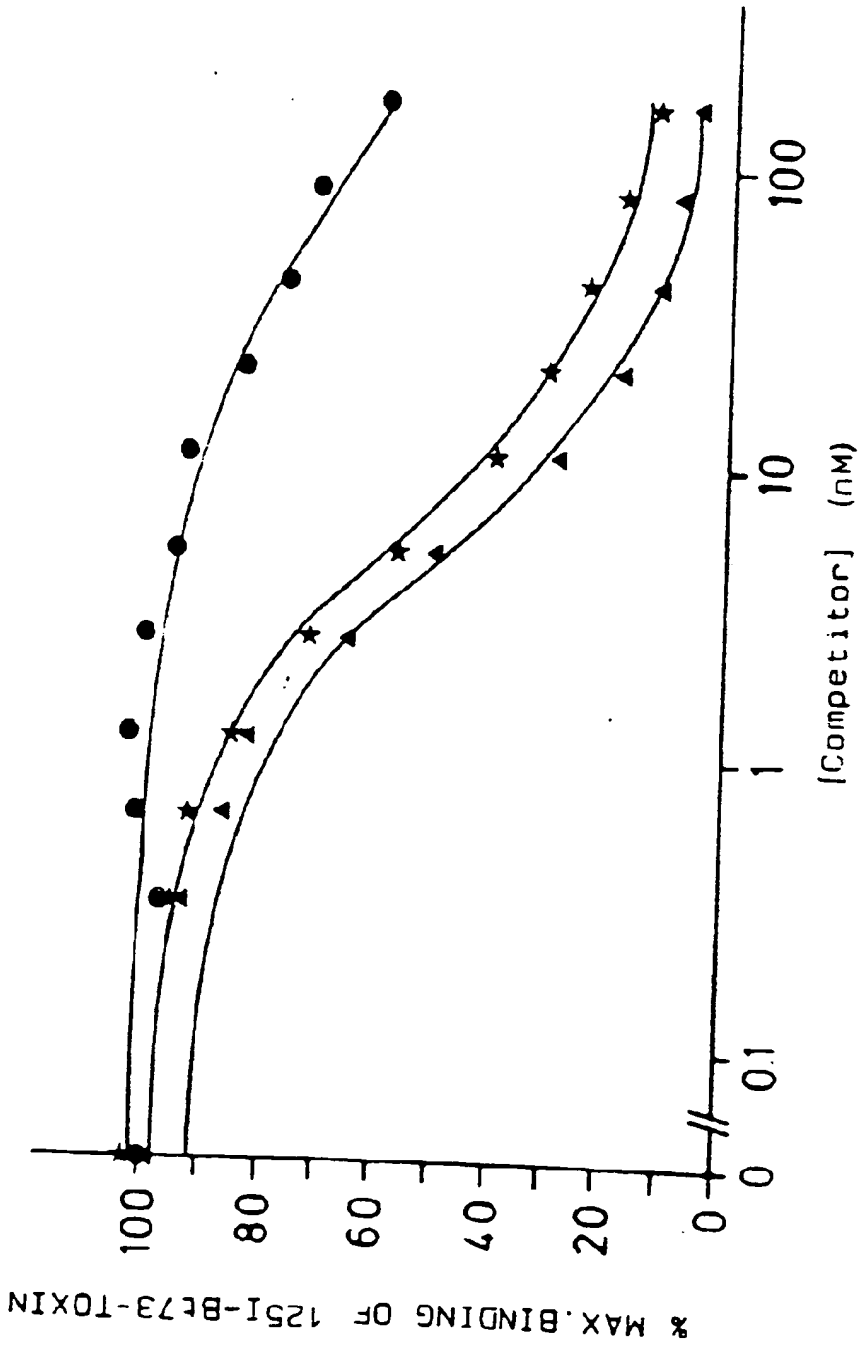

% MAX.BINDING OF 125I-BL73-TOXIN
100
80
60
40
20
0
0
0.1
1
10
100
[Competitor] (nM)

FIGURE 7

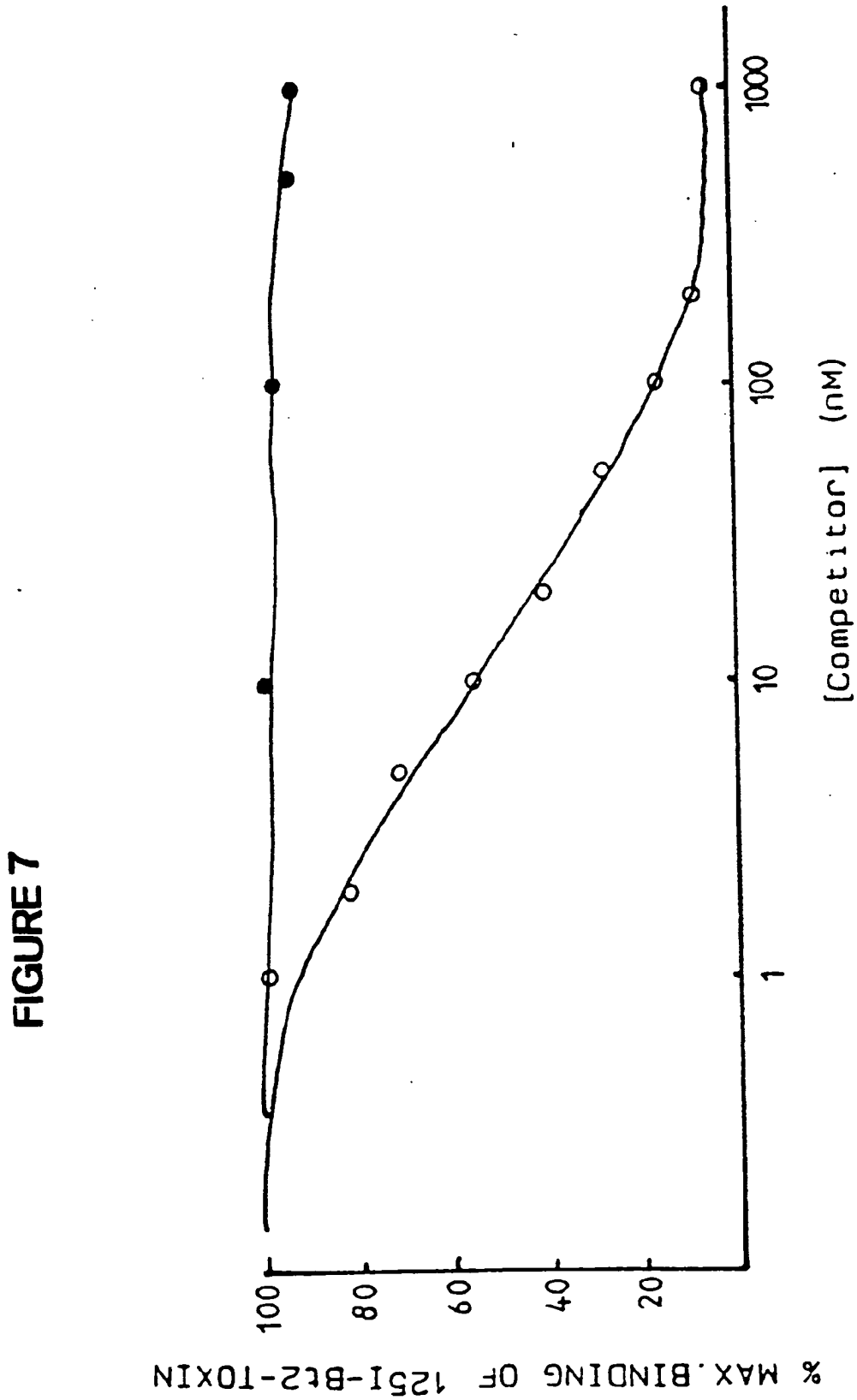

% MAX.BINDING OF 125I-Btc2-TOXIN
100
80
60
40
20
1
10
100
1000
[Competitor] (nM)

FIGURE 8

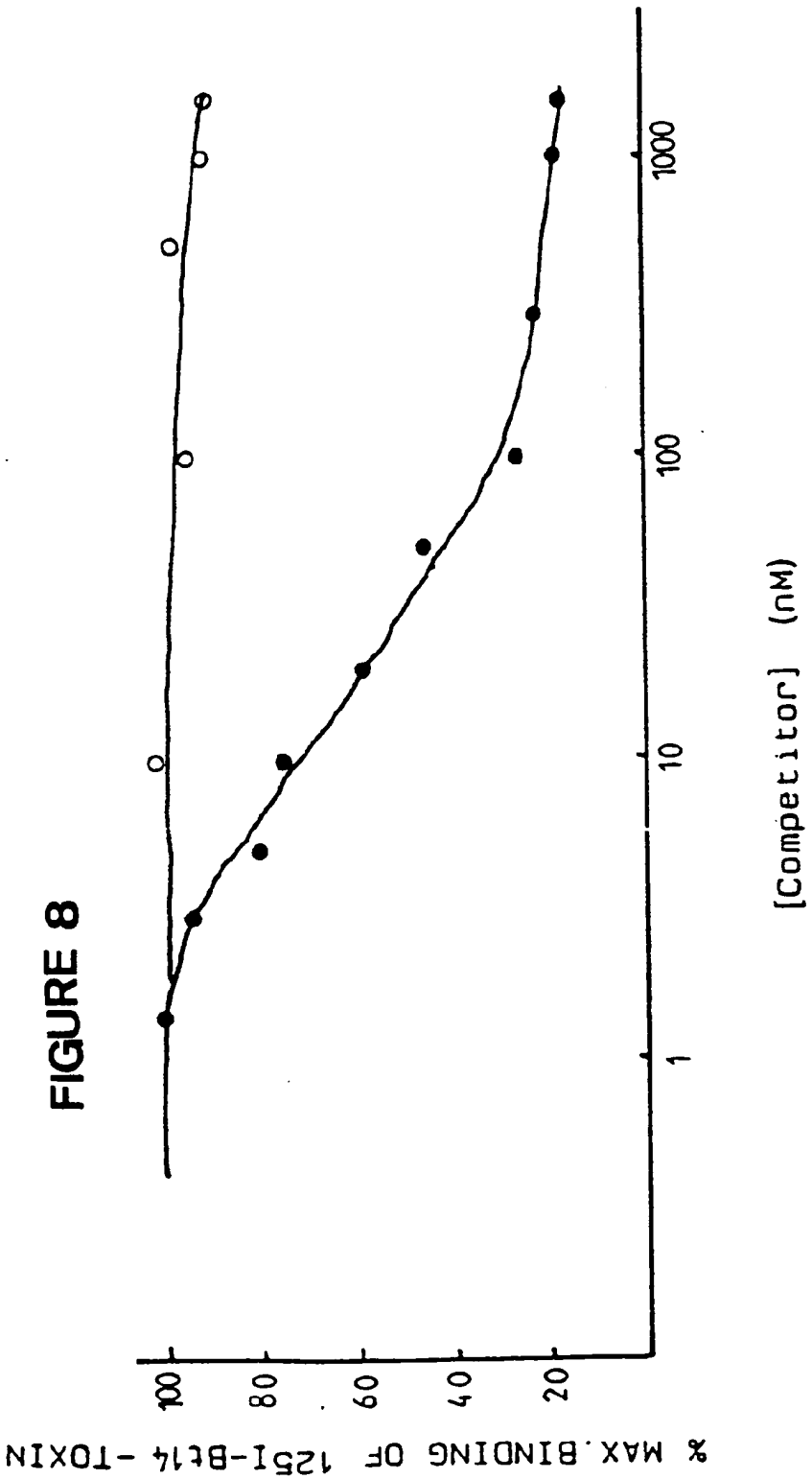

% MAX.BINDING OF 125I-Btl4 -TOXIN
100
80
60
40
20
1
10
100
1000
[Competitor] (nM)

FIGURE 9

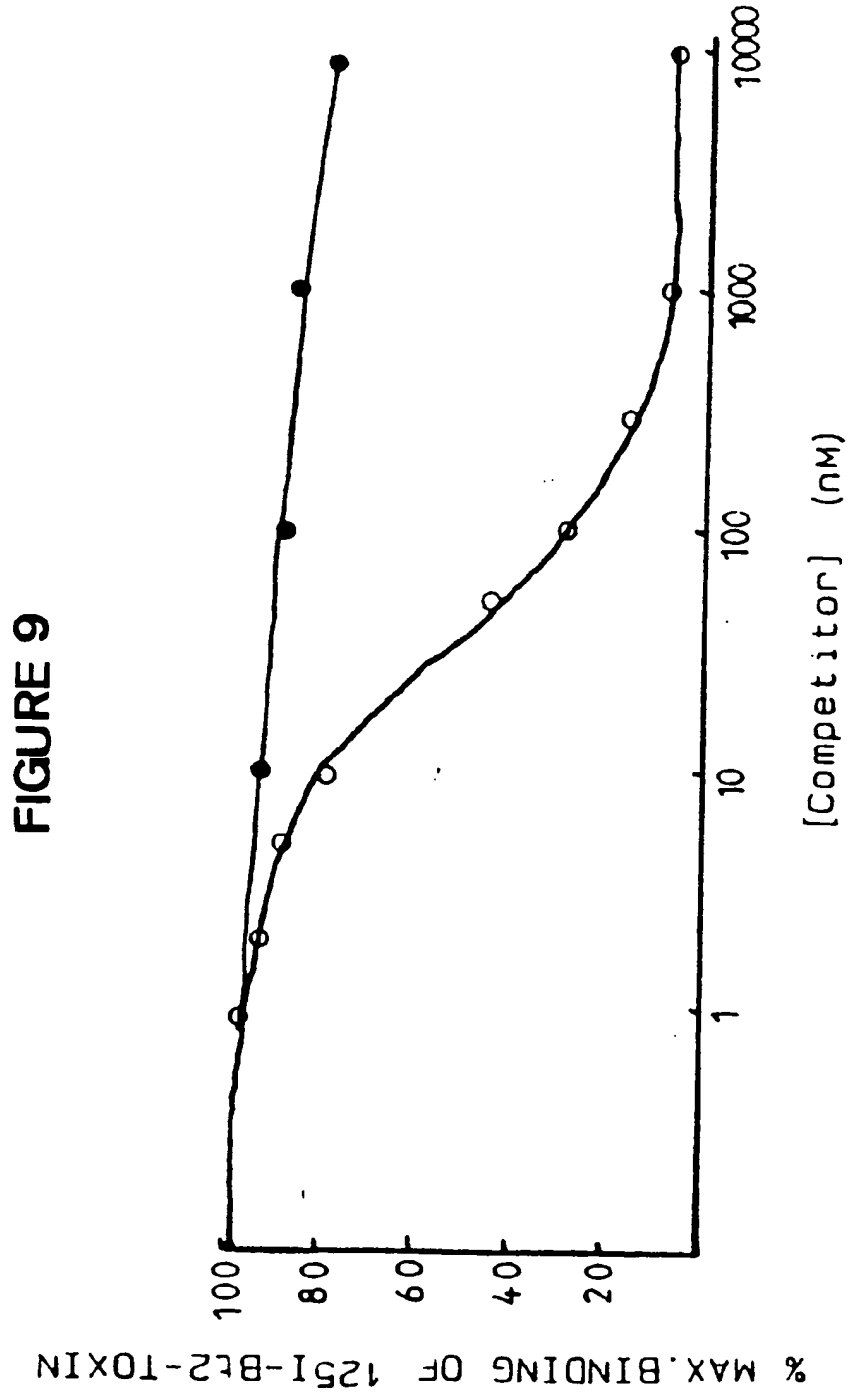

% MAX.BINDING OF 125I-Bt2-TOXIN
100
80
60
40
20
1
10
100
1000
10000
[Competitor] (nM)

FIGURE 10

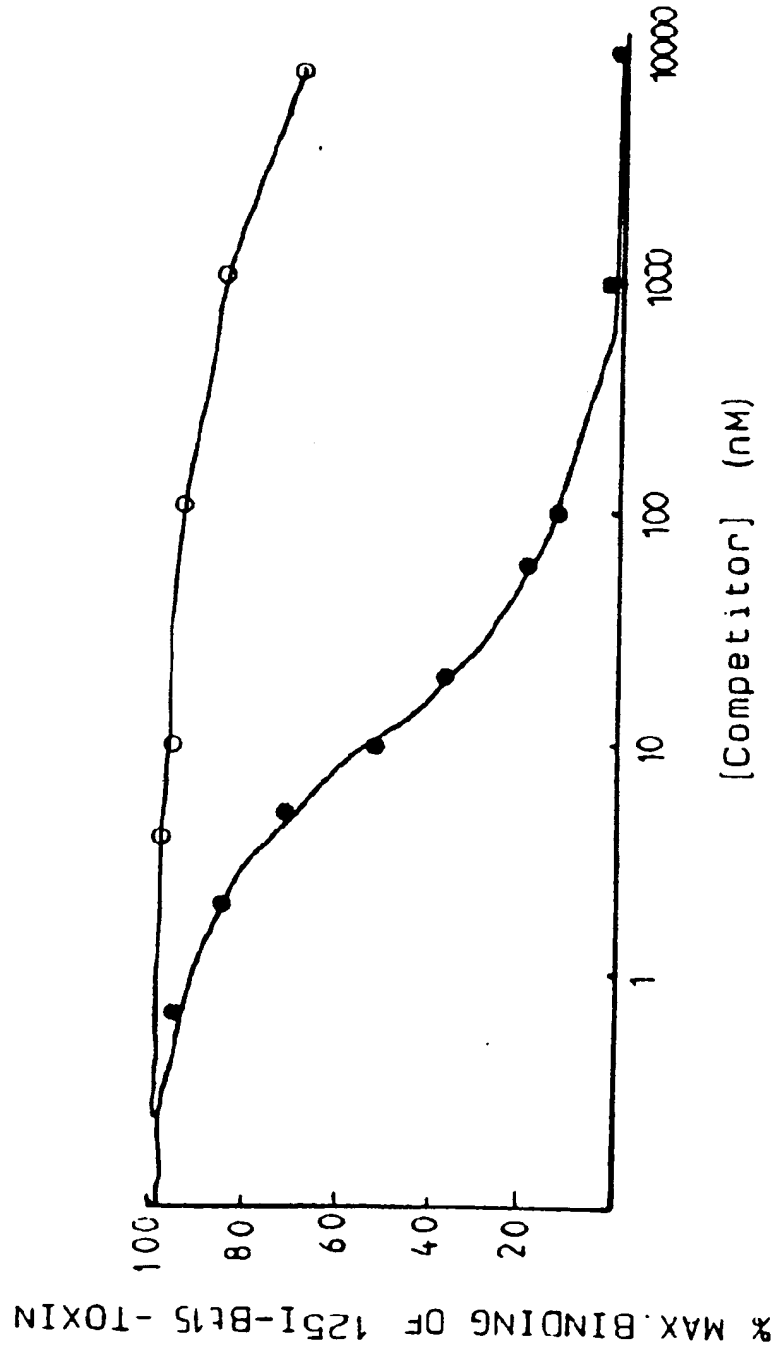

% MAX. BINDING OF 125I-BL15 -TOXIN
100
80
60
40
20
1
10
100
1000
10000
[Competitor] (nM)

FIGURE 11

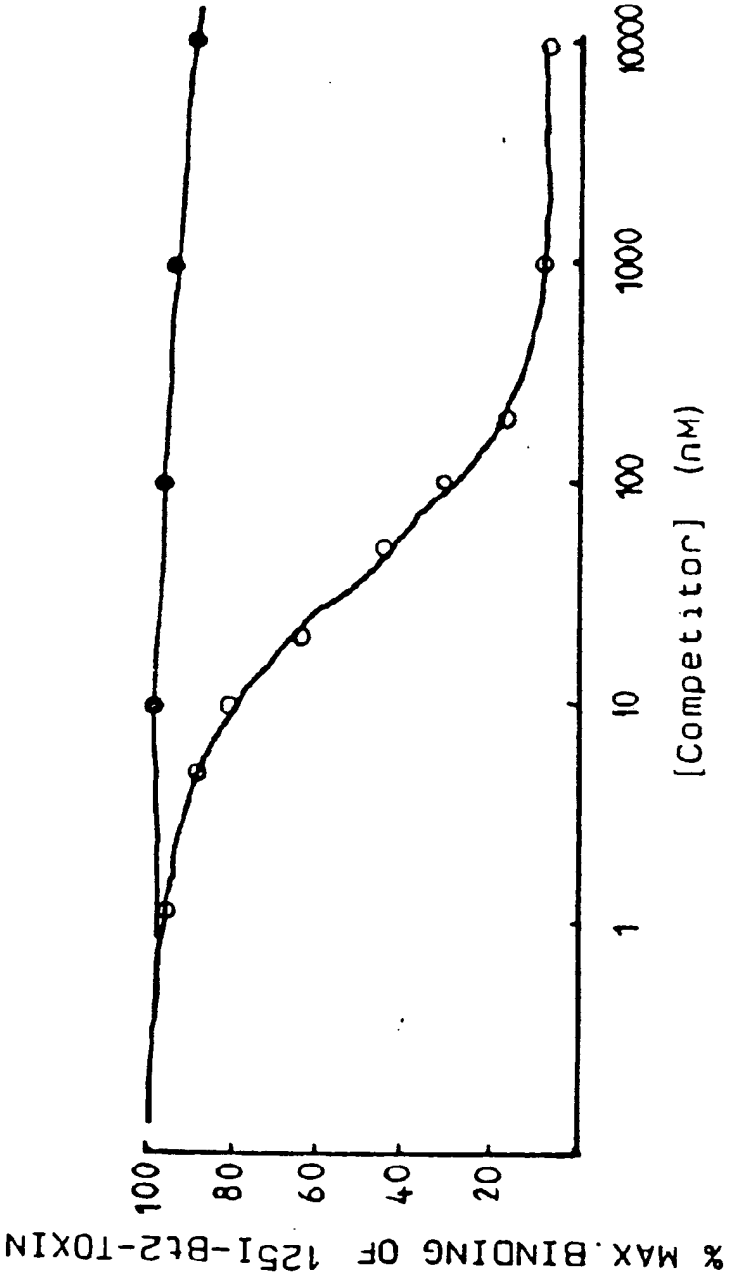

% MAX. BINDING OF 125I-Btx-TOXIN
100
80
60
40
20
1
10
100
1000
10000
[Competitor] (nM)

FIGURE 12

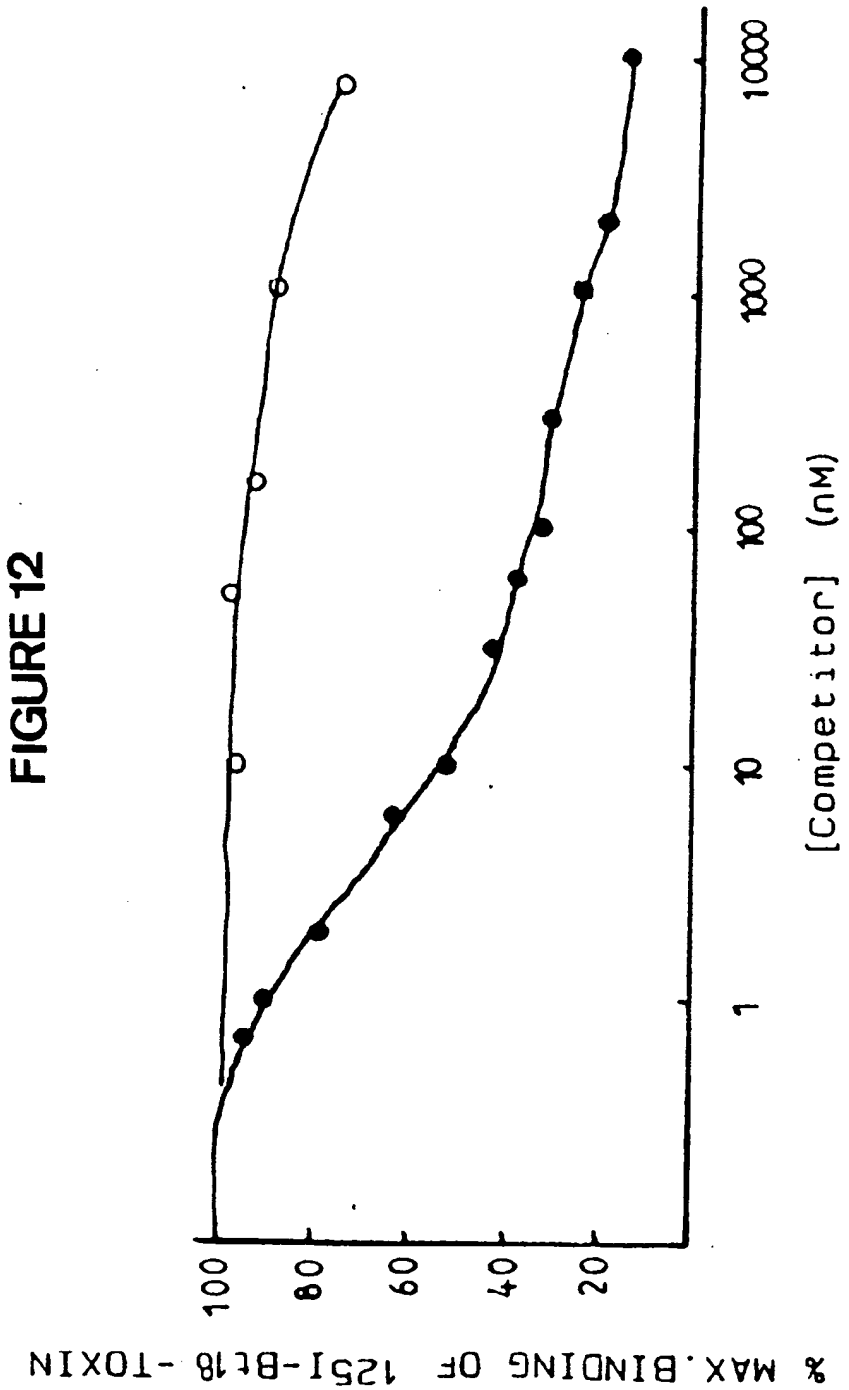

% MAX. BINDING OF 125I-Bt18 -TOXIN
100
80
60
40
20
1
10
100
1000
10000
[Competitor] (nM)

Figure 13

```
        10         20         30         40         50
GGATCTGTTT TAATATAAGG GATTTGTGCC CTTCTCGTTA TATTCTTTTA

        60         70         80         90        100
TTAGCCCCAA AAACTAGTGC AACTAAATAT TTTTATAATT ACACTGATTA

       110        120        130        140        150
AATACTTTAT TTTTGGGAGT AAGATTTATG CTGAAATGTA ATAAAATTCG

       160        170        180        190        200
TTCCATTTTC TGTATTTTCT CATAAAATGT TTCATATGCT TTAAATTGTA

       210        220        230        240        250
GTAAAGAAAA ACAGTACAAA CTTAAAAGGA CTTTAGTAAT TTAATAAAAA

       260        269        278        287
AAGGGGATAG TTT ATG GAA ATA AAT AAT CAA AAC CAA TGT
              MET Glu Ile Asn Asn Gln Asn Gln Cys
```

Figure 13 (Cont. 1)

```
    296         305         314         323
GTG CCT TAC AAT TGT TTA AGT AAT CCT AAG GAG ATA ATA
Val Pro Tyr Asn Cys Leu Ser Asn Pro Lys Glu Ile Ile

332         341         350         359         368
TTA GGC GAG GAA AGG CTA GAA ACA GGG AAT ACT GTA GCA
Leu Gly Glu Glu Arg Leu Glu Thr Gly Asn Thr Val Ala

        377         386         395         404
GAC ATT TCA TTA GGG CTT ATT AAT TTT CTA TAT TCT AAT
Asp Ile Ser Leu Gly Leu Ile Asn Phe Leu Tyr Ser Asn

    413         422         431         440
TTT GTA CCA GGA GGA GGA TTT ATA GTA GGT TTA CTA GAA
Phe Val Pro Gly Gly Gly Phe Ile Val Gly Leu Leu Glu

449         458         467         476         485
TTA ATA TGG GGA TTT ATA GGG CCT TCG CAA TGG GAT ATT
Leu Ile Trp Gly Phe Ile Gly Pro Ser Gln Trp Asp Ile

        494         503         512         521
TTT TTA GCT CAA ATT GAG CAA TTG ATT AGT CAA AGA ATA
Phe Leu Ala Gln Ile Glu Gln Leu Ile Ser Gln Arg Ile
```

Figure 13 (Cont. 2)

```
    530         539         548         557
GAA GAA TTT GCT AGG AAT CAG GCA ATT TCA AGA TTG GAG
Glu Glu Phe Ala Arg Asn Gln Ala Ile Ser Arg Leu Glu

566         575         584         593         602
GGG CTA AGC AAT CTT TAT AAG GTC TAT GTT AGA GCG TTT
Gly Leu Ser Asn Leu Tyr Lys Val Tyr Val Arg Ala Phe

        611         620         629         638
AGC GAC TGG GAG AAA GAT CCT ACT AAT CCT GCT TTA AGG
Ser Asp Trp Glu Lys Asp Pro Thr Asn Pro Ala Leu Arg

    647         656         665         674
GAA GAA ATG CGT ATA CAA TTT AAT GAC ATG AAT AGT GCT
Glu Glu MET Arg Ile Gln Phe Asn Asp MET Asn Ser Ala

683         692         701         710         719
CTC ATA ACG GCT ATT CCA CTT TTT AGA GTT CAA AAT TAT
Leu Ile Thr Ala Ile Pro Leu Phe Arg Val Gln Asn Tyr

        728         737         746         755
GAA GTT GCT CTT TTA TCT GTA TAT GTT CAA GCC GCA AAC
Glu Val Ala Leu Leu Ser Val Tyr Val Gln Ala Ala Asn
```

Figure 13 (Cont. 3)

```
    764         773         782         791
TTA CAT TTA TCT ATT TTA AGG GAT GTT TCA GTT TTC GGA
Leu His Leu Ser Ile Leu Arg Asp Val Ser Val Phe Gly

800         809         818         827         836
GAA AGA TGG GGA TAT GAT ACA GCG ACT ATC AAT AAT CGC
Glu Arg Trp Gly Tyr Asp Thr Ala Thr Ile Asn Asn Arg

        845         854         863         872
TAT AGT GAT CTG ACT AGC CTT ATT CAT GTT TAT ACT AAC
Tyr Ser Asp Leu Thr Ser Leu Ile His Val Tyr Thr Asn

    881         890         899         908
CAT TGT GTG GAT ACG TAT AAT CAG GGA TTA AGG CGT TTG
His Cys Val Asp Thr Tyr Asn Gln Gly Leu Arg Arg Leu

917         926         935         944         953
GAA GGT CGT TTT CTT AGC GAT TGG ATT GTA TAT AAT CGT
Glu Gly Arg Phe Leu Ser Asp Trp Ile Val Tyr Asn Arg

        962         971         980         989
TTC CGG AGA CAA TTG ACA ATT TCA GTA TTA GAT ATT GTT
Phe Arg Arg Gln Leu Thr Ile Ser Val Leu Asp Ile Val
```

Figure 13 (Cont. 4)

```
    998        1007        1016        1025
GCG TTT TTT CCA AAT TAT GAT ATT AGA ACA TAT CCA ATT
Ala Phe Phe Pro Asn Tyr Asp Ile Arg Thr Tyr Pro Ile

1034        1043        1052        1061        1070
CAA ACA GCT ACT CAG CTA ACG AGG GAA GTC TAT CTG GAT
Gln Thr Ala Thr Gln Leu Thr Arg Glu Val Tyr Leu Asp

       1079        1088        1097        1106
TTA CCT TTT ATT AAT GAA AAT CTT TCT CCT GCA GCA AGC
Leu Pro Phe Ile Asn Glu Asn Leu Ser Pro Ala Ala Ser

   1115        1124        1133        1142
TAT CCA ACC TTT TCA GCT GCT GAA AGT GCT ATA ATT AGA
Tyr Pro Thr Phe Ser Ala Ala Glu Ser Ala Ile Ile Arg

1151        1160        1169        1178        1187
AGT CCT CAT TTA GTA GAC TTT TTA AAT AGC TTT ACC ATT
Ser Pro His Leu Val Asp Phe Leu Asn Ser Phe Thr Ile

      1196        1205        1214        1223
TAT ACA GAT AGT CTG GCA CGT TAT GCA TAT TGG GGA GGG
Tyr Thr Asp Ser Leu Ala Arg Tyr Ala Tyr Trp Gly Gly
```

Figure 13 (Cont. 5)

```
   1232        1241        1250        1259
CAC TTG GTA AAT TCT TTC CGC ACA GGA ACC ACT ACT AAT
His Leu Val Asn Ser Phe Arg Thr Gly Thr Thr Thr Asn

1268        1277        1286        1295        1304
TTG ATA AGA TCC CCT TTA TAT GGA AGG GAA GGA AAT ACA
Leu Ile Arg Ser Pro Leu Tyr Gly Arg Glu Gly Asn Thr

       1313        1322        1331        1340
GAG CGC CCC GTA ACT ATT ACC GCA TCA CCT AGC GTA CCA
Glu Arg Pro Val Thr Ile Thr Ala Ser Pro Ser Val Pro

   1349        1358        1367        1376
ATA TTT AGA ACA CTT TCA TAT ATT ACA GGC CTT GAC AAT
Ile Phe Arg Thr Leu Ser Tyr Ile Thr Gly Leu Asp Asn

1385        1394        1403        1412        1421
TCA AAT CCT GTA GCT GGA ATC GAG GGA GTG GAA TTC CAA
Ser Asn Pro Val Ala Gly Ile Glu Gly Val Glu Phe Gln

       1430        1439        1448        1457
AAT ACT ATA AGT AGA AGT ATC TAT CGT AAA AGC GGT CCA
Asn Thr Ile Ser Arg Ser Ile Tyr Arg Lys Ser Gly Pro
```

Figure 13 (Cont. 6)

```
   1466        1475        1484        1493
ATA GAT TCT TTT AGT GAA TTA CCA CCT CAA GAT GCC AGC
Ile Asp Ser Phe Ser Glu Leu Pro Pro Gln Asp Ala Ser

1502        1511        1520        1529        1538
GTA TCT CCT GCA ATT GGG TAT AGT CAC CGT TTA TGC CAT
Val Ser Pro Ala Ile Gly Tyr Ser His Arg Leu Cys His

      1547        1556        1565        1574
GCA ACA TTT TTA GAA CGG ATT AGT GGA CCA AGA ATA GCA
Ala Thr Phe Leu Glu Arg Ile Ser Gly Pro Arg Ile Ala

   1583        1592        1601        1610
GGC ACC GTA TTT TCT TGG ACA CAC CGT AGT GCC AGC CCT
Gly Thr Val Phe Ser Trp Thr His Arg Ser Ala Ser Pro

1619        1628        1637        1646        1655
ACT AAT GAA GTA AGT CCA TCT AGA ATT ACA CAA ATT CCA
Thr Asn Glu Val Ser Pro Ser Arg Ile Thr Gln Ile Pro

      1664        1673        1682        1691
TGG GTA AAG GCG CAT ACT CTT GCA TCT GGT GCC TCC GTC
Trp Val Lys Ala His Thr Leu Ala Ser Gly Ala Ser Val
```

Figure 13 (Cont. 7)

```
   1700        1709        1718        1727
ATT AAA GGT CCT GGA TTT ACA GGT GGA GAT ATT CTG ACT
Ile Lys Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Thr

1736        1745        1754        1763        1772
AGG AAT AGT ATG GGC GAG CTG GGG ACC TTA CGA GTA ACC
Arg Asn Ser MET Gly Glu Leu Gly Thr Leu Arg Val Thr

       1781        1790        1799        1808
TTC ACA GGA AGA TTA CCA CAA AGT TAT TAT ATA CGT TTC
Phe Thr Gly Arg Leu Pro Gln Ser Tyr Tyr Ile Arg Phe

   1817        1826        1835        1844
CGT TAT GCT TCG GTA GCA AAT AGG AGT GGT ACA TTT AGA
Arg Tyr Ala Ser Val Ala Asn Arg Ser Gly Thr Phe Arg

1853        1862        1871        1880        1889
TAT TCA CAG CCA CCT TCG TAT GGA ATT TCA TTT CCA AAA
Tyr Ser Gln Pro Pro Ser Tyr Gly Ile Ser Phe Pro Lys

       1898        1907        1916        1925
ACT ATG GAC GCA GGT GAA CCA CTA ACA TCT CGT TCG TTC
Thr MET Asp Ala Gly Glu Pro Leu Thr Ser Arg Ser Phe
```

Figure 13 (Cont. 8)

```
   1934        1943        1952        1961
GCT CAT ACA ACA CTC TTC ACT CCA ATA ACC TTT TCA CGA
Ala His Thr Thr Leu Phe Thr Pro Ile Thr Phe Ser Arg

1970        1979        1988        1997        2006
GCT CAA GAA GAA TTT GAT CTA TAC ATC CAA TCG GGT GTT
Ala Gln Glu Glu Phe Asp Leu Tyr Ile Gln Ser Gly Val
                                                ---
      2015        2024        2033        2042
TAT ATA GAT CGA ATT GAA TTT ATA CCG GTT ACT GCA ACA
Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Thr Ala Thr
----------------------------------------------------->
   2051        2060        2069        2078
TTT GAG GCA GAA TAT GAT TTA GAA AGA GCG CAA AAG GTG
Phe Glu Ala Glu Tyr Asp Leu Glu Arg Ala Gln Lys Val

2087        2096        2105        2114        2123
GTG AAT GCC CTG TTT ACG TCT ACA AAC CAA CTA GGG CTA
Val Asn Ala Leu Phe Thr Ser Thr Asn Gln Leu Gly Leu

      2132        2141        2150        2159
AAA ACA GAT GTG ACG GAT TAT CAT ATT GAT CAG GTA TCC
Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val Ser
```

Figure 13 (Cont. 9)

```
   2168        2177        2186        2195
AAT CTA GTT GCG TGT TTA TCG GAT GAA TTT TGT CTG GAT
Asn Leu Val Ala Cys Leu Ser Asp Glu Phe Cys Leu Asp

2204        2213        2222        2231        2240
GAA AAG AGA GAA TTG TCC GAG AAA GTT AAA CAT GCA AAG
Glu Lys Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys

      2249        2258        2267        2276
CGA CTC AGT GAT GAG CGG AAT TTA CTT CAA GAT CCA AAC
Arg Leu Ser Asp Glu Arg Asn Leu Leu Gln Asp Pro Asn

   2285        2294        2303        2312
TTC AGA GGG ATC AAT AGG CAA CCA GAC CGT GGC TGG AGA
Phe Arg Gly Ile Asn Arg Gln Pro Asp Arg Gly Trp Arg

2321        2330        2339        2348        2357
GGA AGT ACG GAT ATT ACT ATC CAA GGA GGA GAT GAC GTA
Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp Asp Val

      2366        2375        2384        2393
TTC AAA GAG AAT TAC GTT ACG CTA CCG GGT ACC TTT GAT
Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Phe Asp
```

Figure 13 (Cont. 10)

```
   2402        2411        2420        2429
GAG TGC TAT CCA ACG TAT TTA TAT CAA AAA ATA GAT GAG
Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu

2438        2447        2456        2465        2474
TCG AAA TTA AAA GCC TAT ACC CGT TAT CAA TTA AGA GGG
Ser Lys Leu Lys Ala Tyr Thr Arg Tyr Gln Leu Arg Gly

       2483        2492        2501        2510
TAT ATC GAA GAT AGT CAA GAC TTA GAA ATC TAT TTA ATT
Tyr Ile Glu Asp Ser Gln Asp Leu Glu Ile Tyr Leu Ile

   2519        2528        2537        2546
CGT TAC AAT GCA AAA CAC GAA ATA GTA AAT GTA CCA GGT
Arg Tyr Asn Ala Lys His Glu Ile Val Asn Val Pro Gly

2555        2564        2573        2582        2591
ACA GGA AGT TTA TGG CCT CTT TCT GTA GAA AAT CAA ATT
Thr Gly Ser Leu Trp Pro Leu Ser Val Glu Asn Gln Ile

       2600        2609        2618        2627
GGA CCT TGT GGA GAA CCG AAT CGA TGC GCG CCA CAC CTT
Gly Pro Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu
```

Figure 13 (Cont. 11)

```
   2636        2645        2654        2663
GAA TGG AAT CCT GAT TTA CAC TGT TCC TGC AGA GAC GGG
Glu Trp Asn Pro Asp Leu His Cys Ser Cys Arg Asp Gly

2672        2681        2690        2699        2708
GAA AAA TGT GCA CAT CAT TCT CAT CAT TTC TCT TTG GAC
Glu Lys Cys Ala His His Ser His His Phe Ser Leu Asp

       2717        2726        2735        2744
ATT GAT GTT GGA TGT ACA GAC TTA AAT GAG GAC TTA GGT
Ile Asp Val Gly Cys Thr Asp Leu Asn Glu Asp Leu Gly

   2753        2762        2771        2780
GTA TGG GTG ATA TTC AAG ATT AAG ACG CAA GAT GGC CAC
Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly His

2789        2798        2807        2816        2825
GCA CGA CTA GGG AAT CTA GAG TTT CTC GAA GAG AAA CCA
Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Glu Lys Pro

       2834        2843        2852        2861
TTA TTA GGA GAA GCA CTA GCT CGT GTG AAA AGA GCG GAG
Leu Leu Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu
```

Figure 13 (Cont. 12)

```
   2870        2879        2888        2897
AAA AAA TGG AGA GAC AAA CGC GAA ACA TTA CAA TTG GAA
Lys Lys Trp Arg Asp Lys Arg Glu Thr Leu Gln Leu Glu

2906        2915        2924        2933        2942
ACA ACT ATC GTT TAT AAA GAG GCA AAA GAA TCT GTA GAT
Thr Thr Ile Val Tyr Lys Glu Ala Lys Glu Ser Val Asp

       2951        2960        2969        2978
GCT TTA TTT GTA AAC TCT CAA TAT GAT AGA TTA CAA GCG
Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu Gln Ala

   2987        2996        3005        3014
GAT ACG AAC ATC GCG ATG ATT CAT GCG GCA GAT AAA CGC
Asp Thr Asn Ile Ala MET Ile His Ala Ala Asp Lys Arg

3023        3032        3041        3050        3059
GTT CAT AGA ATT CGA GAA GCG TAT CTG CCG GAG CTG TCT
Val His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser

       3068        3077        3086        3095
GTG ATT CCG GGT GTC AAT GCG GCT ATT TTT GAA GAA TTA
Val Ile Pro Gly Val Asn Ala Ala Ile Phe Glu Glu Leu
```

Figure 13 (Cont. 14)

```
   3338        3347        3356        3365
TAT GGA GAA GGT TGC GTA ACG ATC CAT GAG ATC GAG AAC
Tyr Gly Glu Gly Cys Val Thr Ile His Glu Ile Glu Asn

3374        3383        3392        3401        3410
AAT ACA GAC GAA CTG AAA TTC AAC AAC TGT GTA GAA GAG
Asn Thr Asp Glu Leu Lys Phe Asn Asn Cys Val Glu Glu

       3419        3428        3437        3446
GAA GTA TAT CCA AAC AAC ACG GTA ACG TGT ATT AAT TAT
Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Ile Asn Tyr

   3455        3464        3473        3482
ACT GCG ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT
Thr Ala Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser

3491        3500        3509        3518        3527
CGT AAT CGA GGA TAT GAC GAA GCC TAT GGT AAT AAC CCT
Arg Asn Arg Gly Tyr Asp Glu Ala Tyr Gly Asn Asn Pro

       3536        3545        3554        3563
TCC GTA CCA GCT GAT TAT GCG TCA GTC TAT GAA GAA AAA
Ser Val Pro Ala Asp Tyr Ala Ser Val Tyr Glu Glu Lys
```

Figure 13 (Cont. 13)

```
   3104        3113        3122        3131
GAA GAG CGT ATT TTC ACT GCA TTT TCC CTA TAT GAT GCG
Glu Glu Arg Ile Phe Thr Ala Phe Ser Leu Tyr Asp Ala

3140        3149        3158        3167        3176
AGA AAT ATT ATT AAA AAT GGC GAT TTC AAT AAT GGC TTA
Arg Asn Ile Ile Lys Asn Gly Asp Phe Asn Asn Gly Leu

      3185        3194        3203        3212
TTA TGC TGG AAC GTG AAA GGG CAT GTA GAG GTA GAA GAA
Leu Cys Trp Asn Val Lys Gly His Val Glu Val Glu Glu

   3221        3230        3239        3248
CAA AAC AAT CAC CGT TCA GTC CTG GTT ATC CCA GAA TGG
Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp

3257        3266        3275        3284        3293
GAG GCA GAA GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT
Glu Ala Glu Val Ser Gln Glu Val Arg Val Cys Pro Gly

      3302        3311        3320        3329
CGT GGC TAT ATC CTT CGT GTT ACA GCG TAC AAA GAG GGA
Arg Gly Tyr Ile Leu Arg Val Thr Ala Tyr Lys Glu Gly
```

Figure 13 (Cont. 15)

```
   3572        3581        3590        3599
TCG TAT ACA GAT AGA CGA AGA GAG AAT CCT TGT GAA TCT
Ser Tyr Thr Asp Arg Arg Arg Glu Asn Pro Cys Glu Ser

3608        3617        3626        3635        3644
AAC AGA GGA TAT GGA GAT TAC ACA CCA CTA CCA GCT GGT
Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly

       3653        3662        3671        3680
TAT GTA ACA AAG GAA TTA GAG TAC TTC CCA GAG ACC GAT
Tyr Val Thr Lys Glu Leu Glu Tyr Phe Pro Glu Thr Asp

   3689        3698        3707        3716
AAG GTA TGG ATT GAG ATT GGA GAA ACA GAA GGA ACA TTC
Lys Val Trp Ile Glu Ile Gly Glu Thr Glu Gly Thr Phe

3725        3734        3743        3752        3761
ATC GTG GAC AGC GTG GAA TTA CTC CTT ATG GAG GAA TAG
Ile Val Asp Ser Val Glu Leu Leu Leu MET Glu Glu  .
```

Figure 13 (Cont. 16)

```
      3771        3781        3791        3801        3811
GACCATCCGA GTATAGCAGT TTAATAAATA TTAATTAAAA TAGTAGTCTA

      3821        3831        3841        3851        3861
ACTTCCGTTC CAATTAAATA AGTAAATTAC AGTTGTAAAA AAAAACGAAC

      3871        3881        3891        3901
ATTACTCTTC AAAGAGCGAT GTCCGTTTTT TATATGGTGT GT
```

Figure 14

```
        10         20         30         40         50
AATAGAATCT CAAATCTCGA TGACTGCTTA GTCTTTTTAA TACTGTCTAC

        60         70         80         90        100
TTGACAGGGG TAGGAACATA ATCGGTCAAT TTTAAATATG GGGCATATAT

       110        120        130        140        150
TGATATTTTA TAAAATTTGT TACGTTTTTT GTATTTTTTC ATAAGATGTG

       160        170        180        190        200
TCATATGTAT TAAATCGTGG TAATGAAAAA CAGTATCAAA CTATCAGAAC

       210        220        230        239
TTTGGTAGTT TAATAAAAAA ACGGAGGTAT TTT ATG GAG GAA
                          -----      MET Glu Glu

   248        257        266        275
AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT
Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser

284        293        302        311        320
AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA
Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser
```

Figure 14 (Cont. 1)

```
        329         338         347         356
ACT GGT AAT TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT
Thr Gly Asn Ser Ser Ile Asp Ile Ser Leu Ser Leu Val

    365         374         383         392
CAG TTT CTG GTA TCT AAC TTT GTA CCA GGG GGA GGA TTT
Gln Phe Leu Val Ser Asn Phe Val Pro Gly Gly Gly Phe

401         410         419         428         437
TTA GTT GGA TTA ATA GAT TTT GTA TGG GGA ATA GTT GGC
Leu Val Gly Leu Ile Asp Phe Val Trp Gly Ile Val Gly

        446         455         464         473
CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA CAA
Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu Gln

    482         491         500         509
TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT
Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala

518         527         536         545         554
GCT ATT GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT
Ala Ile Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn
```

Figure 14 (Cont. 2)

```
        563         572         581         590
ATA TAT GTG GAA GCA TTT AAA GAA TGG GAA GAA GAT CCT
Ile Tyr Val Glu Ala Phe Lys Glu Trp Glu Glu Asp Pro

    599         608         617         626
AAT AAT CCA GAA ACC AGG ACC AGA GTA ATT GAT CGC TTT
Asn Asn Pro Glu Thr Arg Thr Arg Val Ile Asp Arg Phe

635         644         653         662         671
CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT CCT TCG
Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile Pro Ser

        680         689         698         707
TTT CGA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT
Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val

    716         725         734         743
TAT GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA
Tyr Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg

752         761         770         779         788
GAT TCT GTA ATT TTT GGA GAA AGA TGG GGA TTG ACA ACG
Asp Ser Val Ile Phe Gly Glu Arg Trp Gly Leu Thr Thr
```

Figure 14 (Cont. 3)

```
        797         806         815         824
ATA AAT GTC AAT GAA AAC TAT AAT AGA CTA ATT AGG CAT
Ile Asn Val Asn Glu Asn Tyr Asn Arg Leu Ile Arg His

    833         842         851         860
ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT ACG TAT AAT
Ile Asp Glu Tyr Ala Asp His Cys Ala Asn Thr Tyr Asn

869         878         887         896         905
CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT
Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp

        914         923         932         941
TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG
Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu

    950         959         968         977
ACT GTA TTA GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC
Thr Val Leu Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp

986         995        1004        1013        1022
AAT AGG AGA TAT CCA ATT CAG CCA GTT GGT CAA CTA ACA
Asn Arg Arg Tyr Pro Ile Gln Pro Val Gly Gln Leu Thr
```

Figure 14 (Cont. 4)

```
      1031        1040        1049        1058
AGG GAA GTT TAT ACG GAC CCA TTA ATT AAT TTT AAT CCA
Arg Glu Val Tyr Thr Asp Pro Leu Ile Asn Phe Asn Pro

   1067        1076        1085        1094
CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC GTT
Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn Val

1103        1112        1121        1130        1139
ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT
MET Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp

      1148        1157        1166        1175
ATA TTG AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT
Ile Leu Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser

   1184        1193        1202        1211
GTT GGA CGC AAT TTT TAT TGG GGA GGA CAT CGA GTA ATA
Val Gly Arg Asn Phe Tyr Trp Gly Gly His Arg Val Ile

1220        1229        1238        1247        1256

TCT AGC CTT ATA GGA GGT GGT AAC ATA ACA TCT CCT ATA
Ser Ser Leu Ile Gly Gly Gly Asn Ile Thr Ser Pro Ile
```

Figure 14 (Cont. 5)

```
      1265        1274        1283        1292
TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA TCC TTT
Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg Ser Phe

   1301        1310        1319        1328
ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT
Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro

1337        1346        1355        1364        1373
ACT TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA
Thr Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro

      1382        1391        1400        1409
TTT AAT TTA CGT GGT GTT GAA GGA GTA GAA TTT TCT ACA
Phe Asn Leu Arg Gly Val Glu Gly Val Glu Phe Ser Thr

   1418        1427        1436        1445
CCT ACA AAT AGC TTT ACG TAT CGA GGA AGA GGT ACG GTT
Pro Thr Asn Ser Phe Thr Tyr Arg Gly Arg Gly Thr Val

1454        1463        1472        1481        1490
GAT TCT TTA ACT GAA TTA CCG CCT GAG GAT AAT AGT GTG
Asp Ser Leu Thr Glu Leu Pro Pro Glu Asp Asn Ser Val
```

Figure 14 (Cont. 6)

```
      1499        1508        1517        1526
CCA CCT CGC GAA GGA TAT AGT CAT CGT TTA TGT CAT GCA
Pro Pro Arg Glu Gly Tyr Ser His Arg Leu Cys His Ala

   1535        1544        1553        1562
ACT TTT GTT CAA AGA TCT GGA ACA CCT TTT TTA ACA ACT
Thr Phe Val Gln Arg Ser Gly Thr Pro Phe Leu Thr Thr

1571        1580        1589        1598        1607
GGT GTA GTA TTT TCT TGG ACG CAT CGT AGT GCA ACT CTT
Gly Val Val Phe Ser Trp Thr His Arg Ser Ala Thr Leu

      1616        1625        1634        1643
ACA AAT ACA ATT GAT CCA GAG AGA ATT AAT CAA ATA CCT
Thr Asn Thr Ile Asp Pro Glu Arg Ile Asn Gln Ile Pro

   1652        1661        1670        1679
TTA GTG AAA GGA TTT AGA GTT TGG GGG GGC ACC TCT GTC
Leu Val Lys Gly Phe Arg Val Trp Gly Gly Thr Ser Val

1688        1697        1706        1715        1724
ATT ACA GGA CCA GGA TTT ACA GGA GGG GAT ATC CTT CGA
Ile Thr Gly Pro Gly Phe Thr Gly Gly Asp Ile Leu Arg
```

Figure 14 (Cont. 7)

```
      1733        1742        1751        1760
AGA AAT ACC TTT GGT GAT TTT GTA TCT CTA CAA GTC AAT
Arg Asn Thr Phe Gly Asp Phe Val Ser Leu Gln Val Asn

   1769        1778        1787        1796
ATT AAT TCA CCA ATT ACC CAA AGA TAC CGT TTA AGA TTT
Ile Asn Ser Pro Ile Thr Gln Arg Tyr Arg Leu Arg Phe

1805        1814        1823        1832        1841
CGT TAC GCT TCC AGT AGG GAT GCA CGA GTT ATA GTA TTA
Arg Tyr Ala Ser Ser Arg Asp Ala Arg Val Ile Val Leu

      1850        1859        1868        1877
ACA GGA GCG GCA TCC ACA GGA GTG GGA GGC CAA GTT AGT
Thr Gly Ala Ala Ser Thr Gly Val Gly Gly Gln Val Ser

   1886        1895        1904        1913
GTA AAT ATG CCT CTT CAG AAA ACT ATG GAA ATA GGG GAG
Val Asn MET Pro Leu Gln Lys Thr MET Glu Ile Gly Glu

1922        1931        1940        1949        1958
AAC TTA ACA TCT AGA ACA TTT AGA TAT ACC GAT TTT AGT
Asn Leu Thr Ser Arg Thr Phe Arg Tyr Thr Asp Phe Ser
```

Figure 14 (Cont. 8)

```
      1967        1976        1985        1994
AAT CCT TTT TCA TTT AGA GCT AAT CCA GAT ATA ATT GGG
Asn Pro Phe Ser Phe Arg Ala Asn Pro Asp Ile Ile Gly

   2003        2012        2021        2030
ATA AGT GAA CAA CCT CTA TTT GGT GCA GGT TCT ATT AGT
Ile Ser Glu Gln Pro Leu Phe Gly Ala Gly Ser Ile Ser

2039        2048        2057        2066        2075
AGC GGT GAA CTT TAT ATA GAT AAA ATT GAA ATT ATT CTA
Ser Gly Glu Leu Tyr Ile Asp Lys Ile Glu Ile Ile Leu

      2084        2093        2102        2111
GCA GAT GCA ACA TTT GAA GCA GAA TCT GAT TTA GAA AGA
Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp Leu Glu Arg

   2120        2129        2138        2147
GCA CAA AAG GCG GTG AAT GCC CTG TTT ACT TCT TCC AAT
Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn

2156        2165        2174        2183        2192
CAA ATC GGG TTA AAA ACC GAT GTG ACG GAT TAT CAT ATT
Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile
```

Figure 14 (Cont. 9)

```
      2201        2210        2219        2228
GAT CAA GTA TCC AAT TTA GTG GAT TGT TTA TCA GAT GAA
Asp Gln Val Ser Asn Leu Val Asp Cys Leu Ser Asp Glu

   2237        2246        2255        2264
TTT TGT CTG GAT GAA AAG CGA GAA TTG TCC GAG AAA GTC
Phe Cys Leu Asp Glu Lys Arg Glu Leu Ser Glu Lys Val

2273        2282        2291        2300        2309
AAA CAT GCG AAG CGA CTC AGT GAT GAG CGG AAT TTA CTT
Lys His Ala Lys Arg Leu Ser Asp Glu Arg Asn Leu Leu

      2318        2327        2336        2345
CAA GAT CCA AAC TTC AGA GGG ATC AAT AGA CAA CCA GAC
Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro Asp

   2354        2363        2372        2381
CGT GGC TGG AGA GGA AGT ACA GAT ATT ACC ATC CAA GGA
Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly

2390        2399        2408        2417        2426
GGA GAT GAC GTA TTC AAA GAG AAT TAC GTC ACA CTA CCG
Gly Asp Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro
```

Figure 14 (Cont. 10)

```
      2435        2444        2453        2462
GGT ACC GTT GAT GAG TGC TAT CCA ACG TAT TTA TAT CAG
Gly Thr Val Asp Glu Cys Tyr Pro Thr Tyr Leu Tyr Gln

   2471        2480        2489        2498
AAA ATA GAT GAG TCG AAA TTA AAA GCT TAT ACC CGT TAT
Lys Ile Asp Glu Ser Lys Leu Lys Ala Tyr Thr Arg Tyr

2507        2516        2525        2534        2543
GAA TTA AGA GGG TAT ATC GAA GAT AGT CAA GAC TTA GAA
Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp Leu Glu

      2552        2561        2570        2579
ATC TAT TTG ATC CGT TAC AAT GCA AAA CAC GAA ATA GTA
Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val

   2588        2597        2606        2615
AAT GTG CCA GGC ACG GGT TCC TTA TGG CCG CTT TCA GCC
Asn Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala

2624        2633        2642        2651        2660
CAA AGT CCA ATC GGA AAG TGT GGA GAA CCG AAT CGA TGC
Gln Ser Pro Ile Gly Lys Cys Gly Glu Pro Asn Arg Cys
```

Figure 14 (Cont. 11)

```
      2669        2678        2687        2696
GCG CCA CAC CTT GAA TGG AAT CCT GAT CTA GAT TGT TCC
Ala Pro His Leu Glu Trp Asn Pro Asp Leu Asp Cys Ser

   2705        2714        2723        2732
TGC AGA GAC GGG GAA AAA TGT GCA CAT CAT TCC CAT CAT
Cys Arg Asp Gly Glu Lys Cys Ala His His Ser His His

2741        2750        2759        2768        2777
TTC ACC TTG GAT ATT GAT GTT GGA TGT ACA GAC TTA AAT
Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn

      2786        2795        2804        2813
GAG GAC TTA GGT GTA TGG GTG ATA TTC AAG ATT AAG ACG
Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr

   2822        2831        2840        2849
CAA GAT GGC CAT GCA AGA CTA GGG AAT CTA GAG TTT CTC
Gln Asp Gly His Ala Arg Leu Gly Asn Leu Glu Phe Leu

2858        2867        2876        2885        2894
GAA GAG AAA CCA TTA TTA GGG GAA GCA CTA GCT CGT GTG
Glu Glu Lys Pro Leu Leu Gly Glu Ala Leu Ala Arg Val
```

Figure 14 (Cont. 12)

```
      2903        2912        2921        2930
AAA AGA GCG GAG AAG AAG TGG AGA GAC AAA CGA GAG AAA
Lys Arg Ala Glu Lys Lys Trp Arg Asp Lys Arg Glu Lys

   2939        2948        2957        2966
CTG CAG TTG GAA ACA AAT ATT GTT TAT AAA GAG GCA AAA
Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala Lys

2975        2984        2993        3002        3011
GAA TCT GTA GAT GCT TTA TTT GTA AAC TCT CAA TAT GAT
Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp

      3020        3029        3038        3047
AGA TTA CAA GTG GAT ACG AAC ATC GCG ATG ATT CAT GCG
Arg Leu Gln Val Asp Thr Asn Ile Ala MET Ile His Ala

   3056        3065        3074        3083
GCA GAT AAA CGC GTT CAT AGA ATC CGG GAA GCG TAT CTG
Ala Asp Lys Arg Val His Arg Ile Arg Glu Ala Tyr Leu

3092        3101        3110        3119        3128
CCA GAG TTG TCT GTG ATT CCA GGT GTC AAT GCG GCC ATT
Pro Glu Leu Ser Val Ile Pro Gly Val Asn Ala Ala Ile
```

Figure 14 (Cont. 13)

```
      3137        3146        3155        3164
TTC GAA GAA TTA GAG GGA CGT ATT TTT ACA GCG TAT TCC
Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala Tyr Ser

   3173        3182        3191        3200
TTA TAT GAT GCG AGA AAT GTC ATT AAA AAT GGC GAT TTC
Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe

3209        3218        3227        3236        3245
AAT AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA
Asn Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val

      3254        3263        3272        3281
GAT GTA GAA GAG CAA AAC AAC CAC CGT TCG GTC CTT GTT
Asp Val Glu Glu Gln Asn Asn His Arg Ser Val Leu Val

   3290        3299        3308        3317
ATC CCA GAA TGG GAG GCA GAA GTG TCA CAA GAG GTT CGT
Ile Pro Glu Trp Glu Ala Glu Val Ser Gln Glu Val Arg

3326        3335        3344        3353        3362
GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT GTC ACA GCA
Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg Val Thr Ala
```

Figure 14 (Cont. 14)

```
      3371        3380        3389        3398
TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT
Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His

   3407        3416        3425        3434
GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC
Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn

3443        3452        3461        3470        3479
TGT GTA GAA GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG
Cys Val Glu Glu Glu Val Tyr Pro Asn Asn Thr Val Thr

      3488        3497        3506        3515
TGT AAT AAT TAT ACT GGG ACT CAA GAA GAA TAT GAG GGT
Cys Asn Asn Tyr Thr Gly Thr Gln Glu Glu Tyr Glu Gly

   3524        3533        3542        3551
ACG TAC ACT TCT CGT AAT CAA GGA TAT GAC GAA GCC TAT
Thr Tyr Thr Ser Arg Asn Gln Gly Tyr Asp Glu Ala Tyr

3560        3569        3578        3587        3596
GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA GTC
Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser Val
```

Figure 14 (Cont. 15)

```
      3605        3614        3623        3632
TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT
Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn

   3641        3650        3659        3668
CCT TGT GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA
Pro Cys Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro

3677        3686        3695        3704        3713
CTA CCG GCT GGT TAT GTA ACA AAG GAT TTA GAG TAC TTC
Leu Pro Ala Gly Tyr Val Thr Lys Asp Leu Glu Tyr Phe

      3722        3731        3740        3749
CCA GAG ACC GAT AAG GTA TGG ATT GAG ATC GGA GAA ACA
Pro Glu Thr Asp Lys Val Trp Ile Glu Ile Gly Glu Thr

   3758        3767        3776        3785
GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA CTC CTT
Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu Leu Leu

3794        3803        3813        3823        3833
ATG GAG GAA TAA GATACGTTAT AAAATGTAAC GTATGCAAAT
MET Glu Glu  .
```

Figure 14 (Cont. 16)

```
      3843        3853        3863        3873        3883
AAAGAATGAT TACTGACCTA TATTAACAGA TAAATAAGAA AATTTTTATA

      3893        3903        3913        3923
CGAATAAAAA ACGGACATCA CTCTTAAGAG AATGATGTCC
```

FIGURE 15

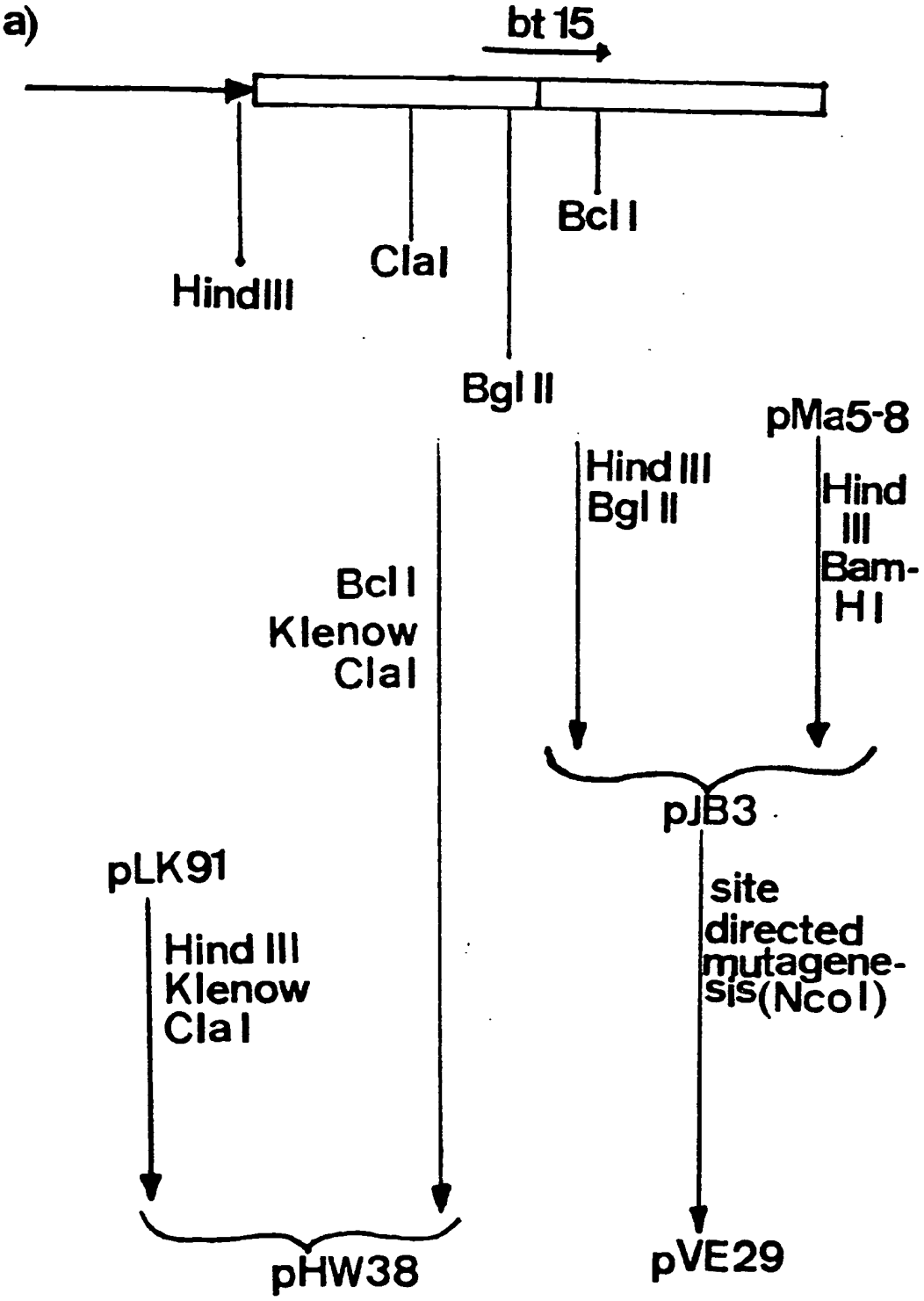
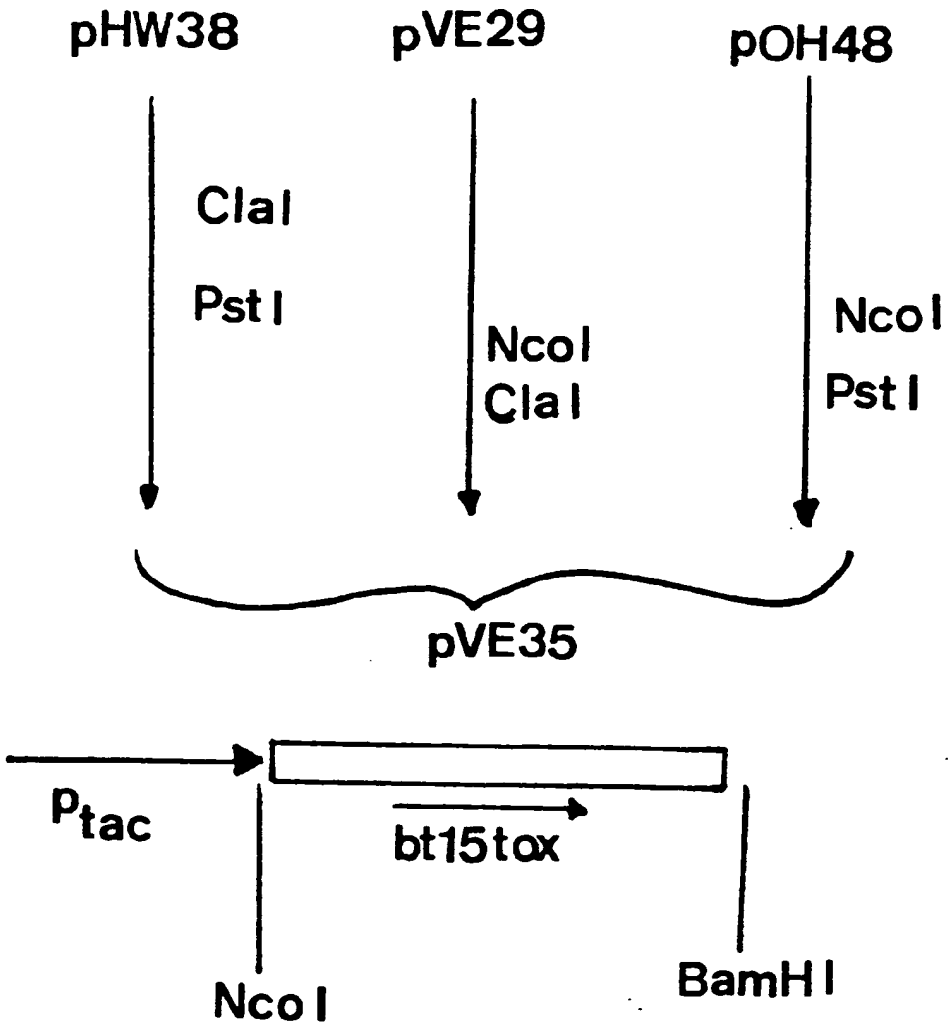

a)
bt 15
HindIII
ClaI
BglII
BclI
pMa5-8
Hind III
BglII
Hind III
Bam-HI
BclI
Klenow
ClaI
pJB3
pLK91
Hind III
Klenow
ClaI
site directed mutagene-sis(NcoI)
pHW38
pVE29

Fig. 15 (cont)

b)


pHW38
pVE29
pOH48
ClaI
PstI
NcoI
ClaI
NcoI
PstI
pVE35
Ptac
bt15tox
NcoI
BamHI

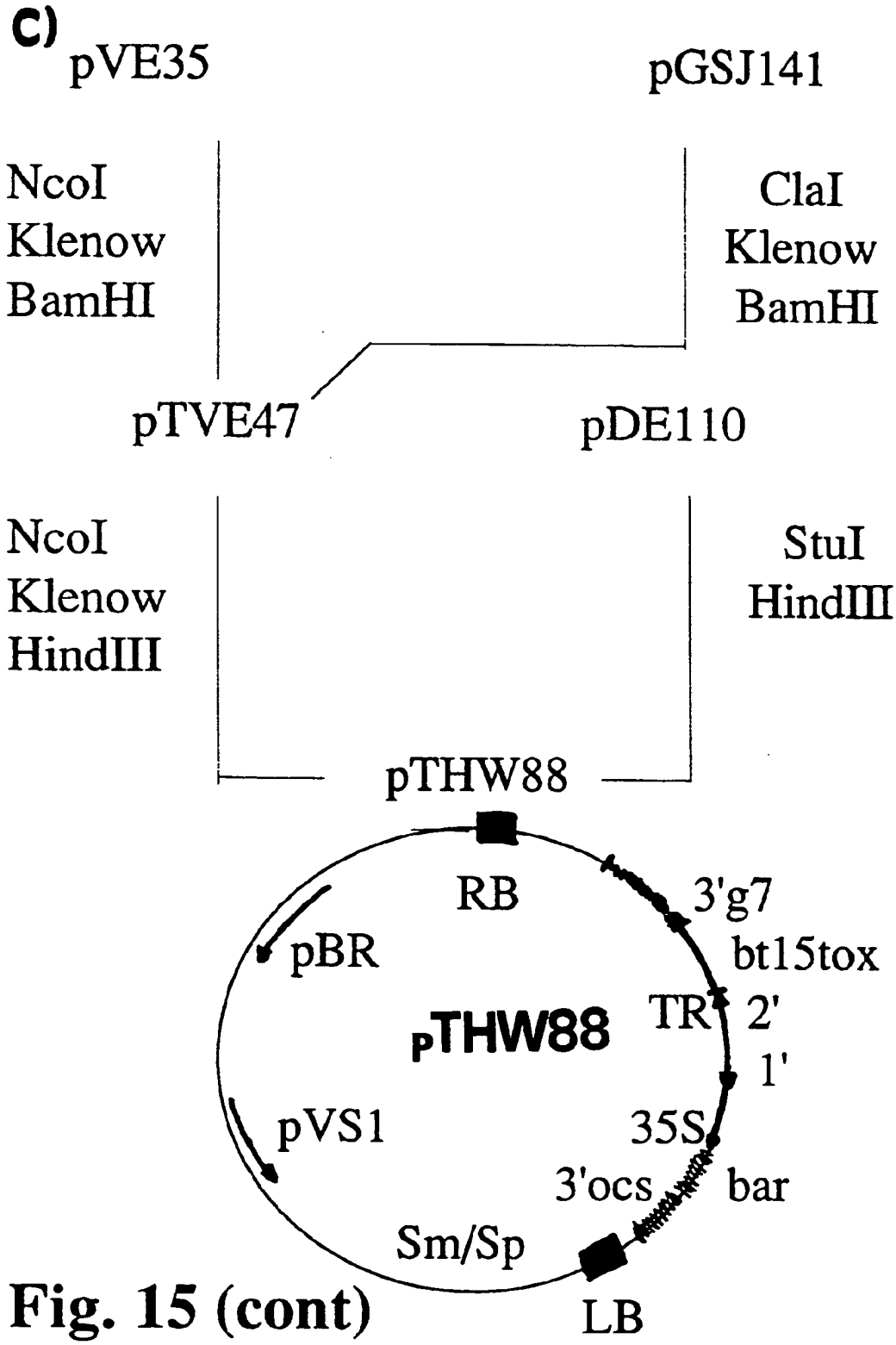

C)
pVE35
pGSJ141
NcoI
Klenow
BamHI
ClaI
Klenow
BamHI
pTVE47
pDE110
NcoI
Klenow
HindIII
StuI
HindIII
pTHW88
RB
3'g7
pBR
bt15tox
TR
2'
pTHW88
1'
pVS1
35S
3'ocs
bar
Sm/Sp
LB

Fig. 15 (cont)

FIGURE 16
a)

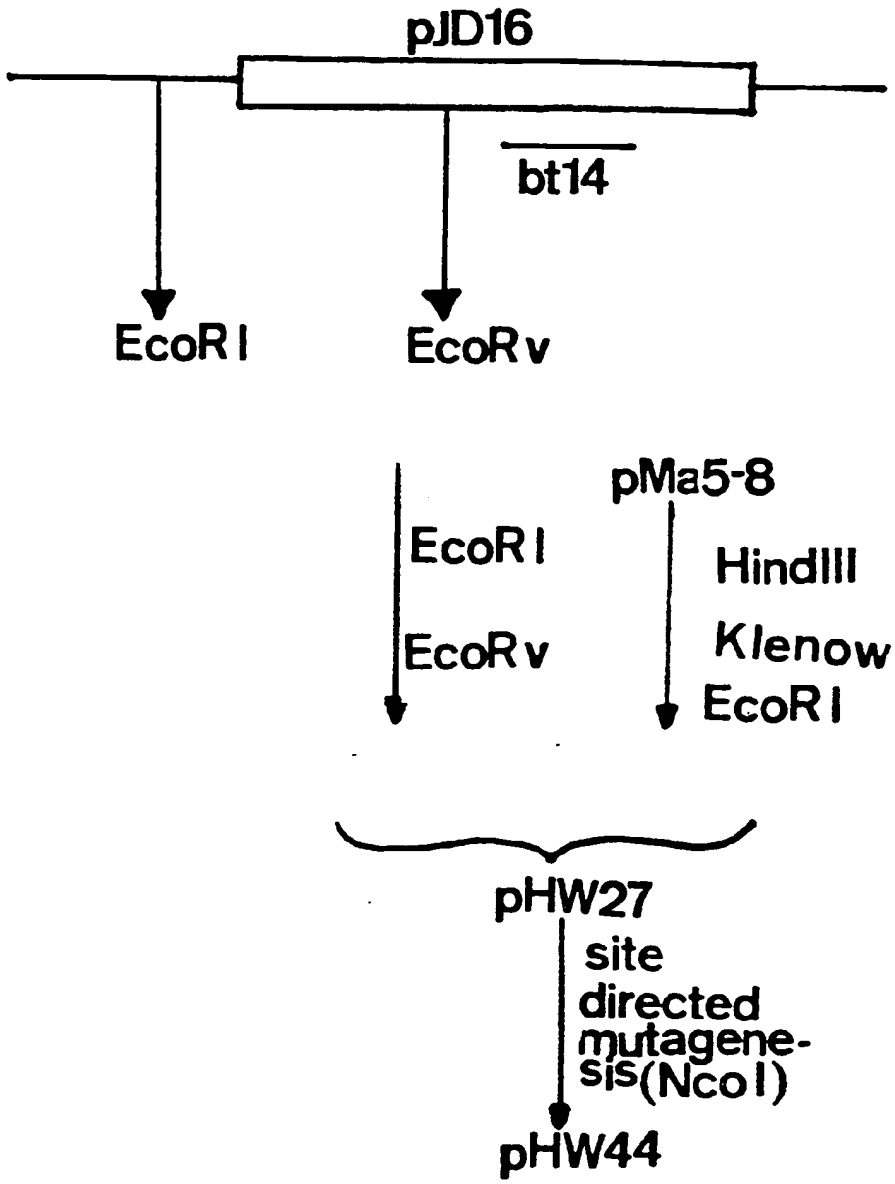
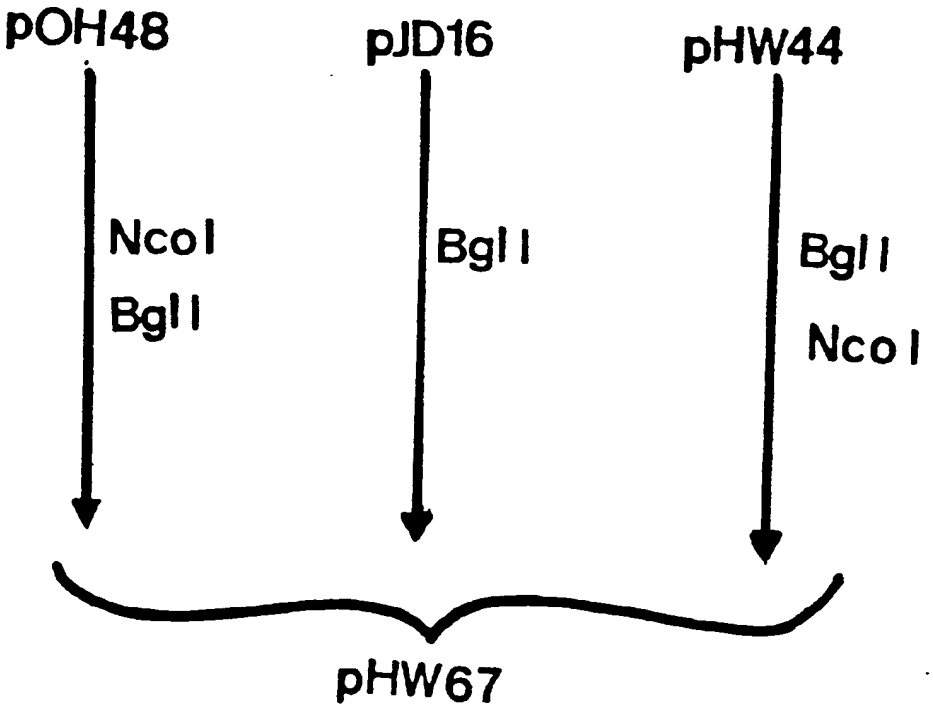

pJD16
bt14
EcoR I
EcoR v
pMa5-8
EcoR I
EcoR v
Hind III
Klenow
EcoR I
pHW27
site
directed
mutagene-
sis(Nco I)
pHW44

FIGURE 16

b)


pOH48
pJD16
pHW44
NcoI
BglI
BglI
BglI
NcoI
pHW67

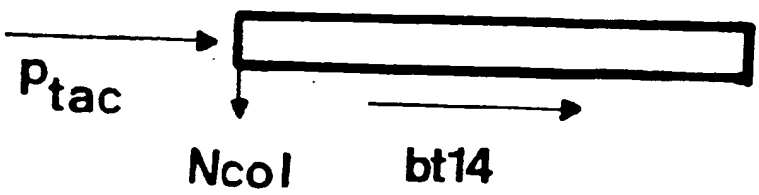

Ptac
NcoI
bt14

FIGURE 16

c)

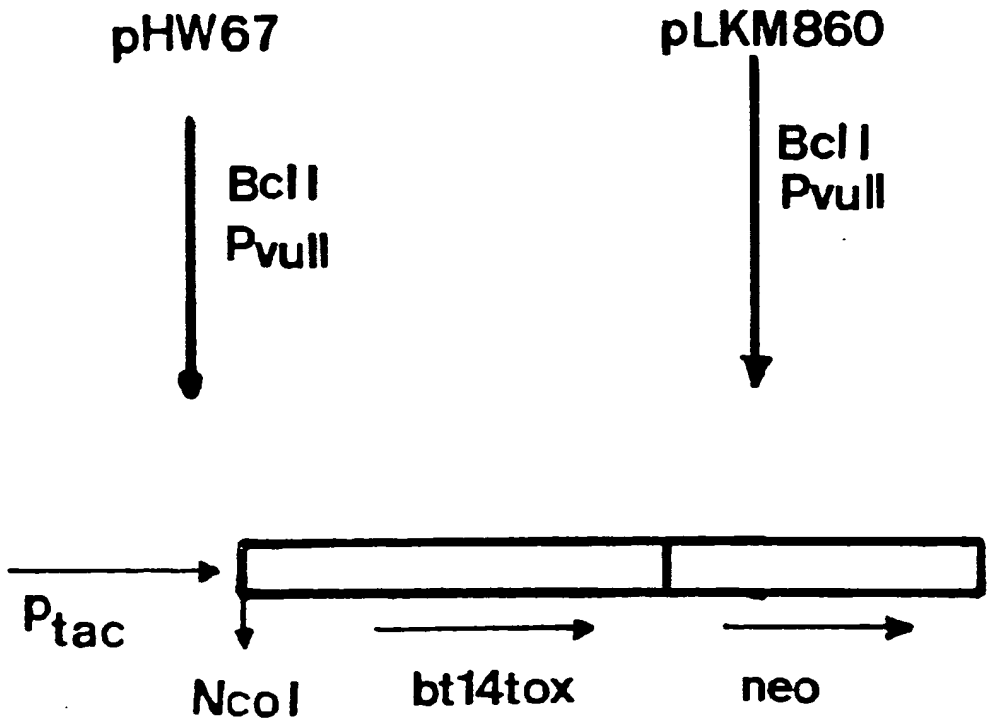


FIGURE 16 (CONT)

d)

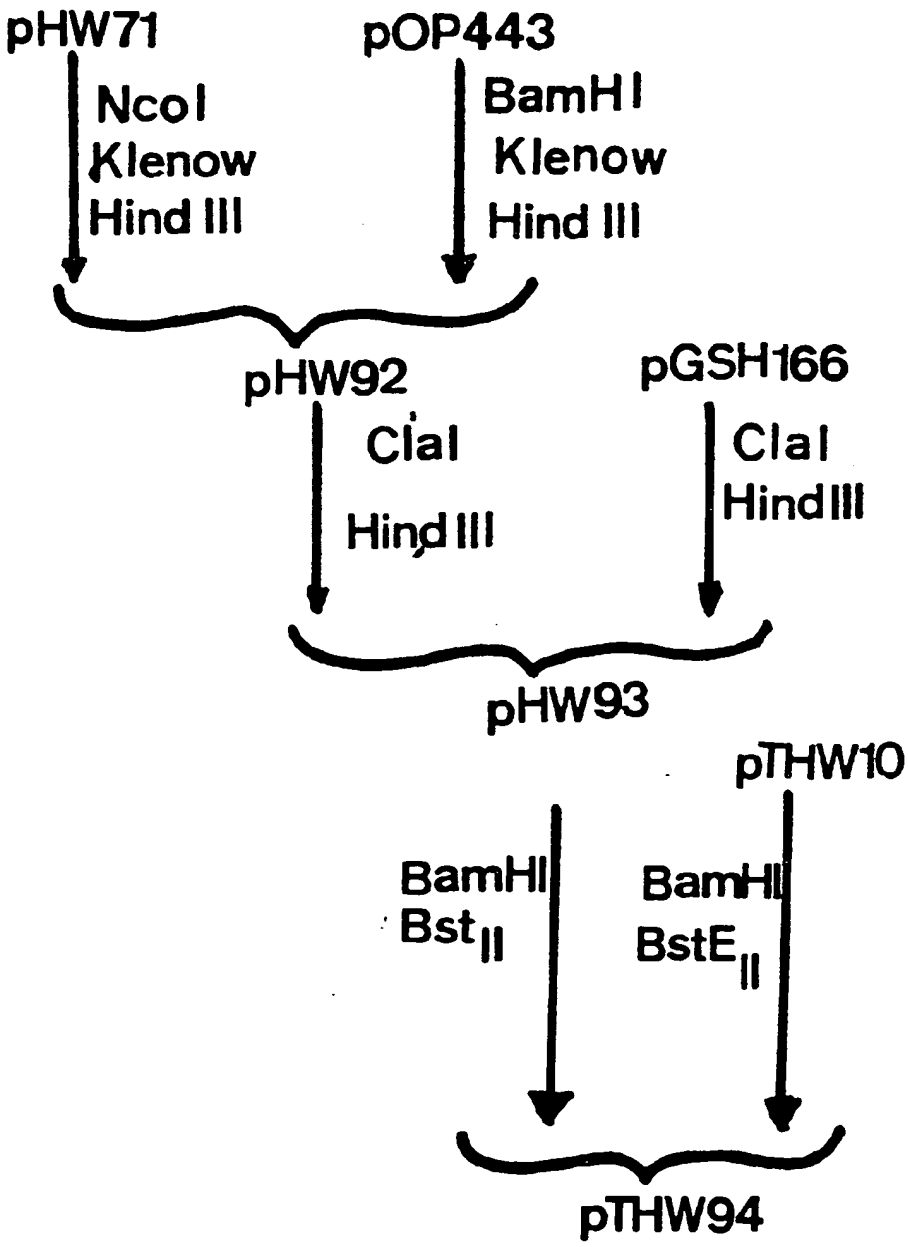
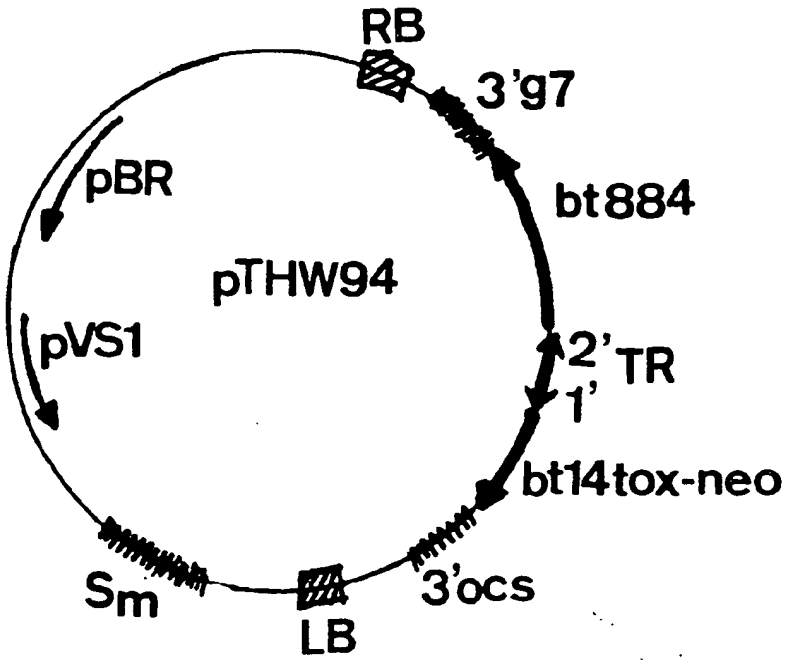


FIGURE 16 (CONT)



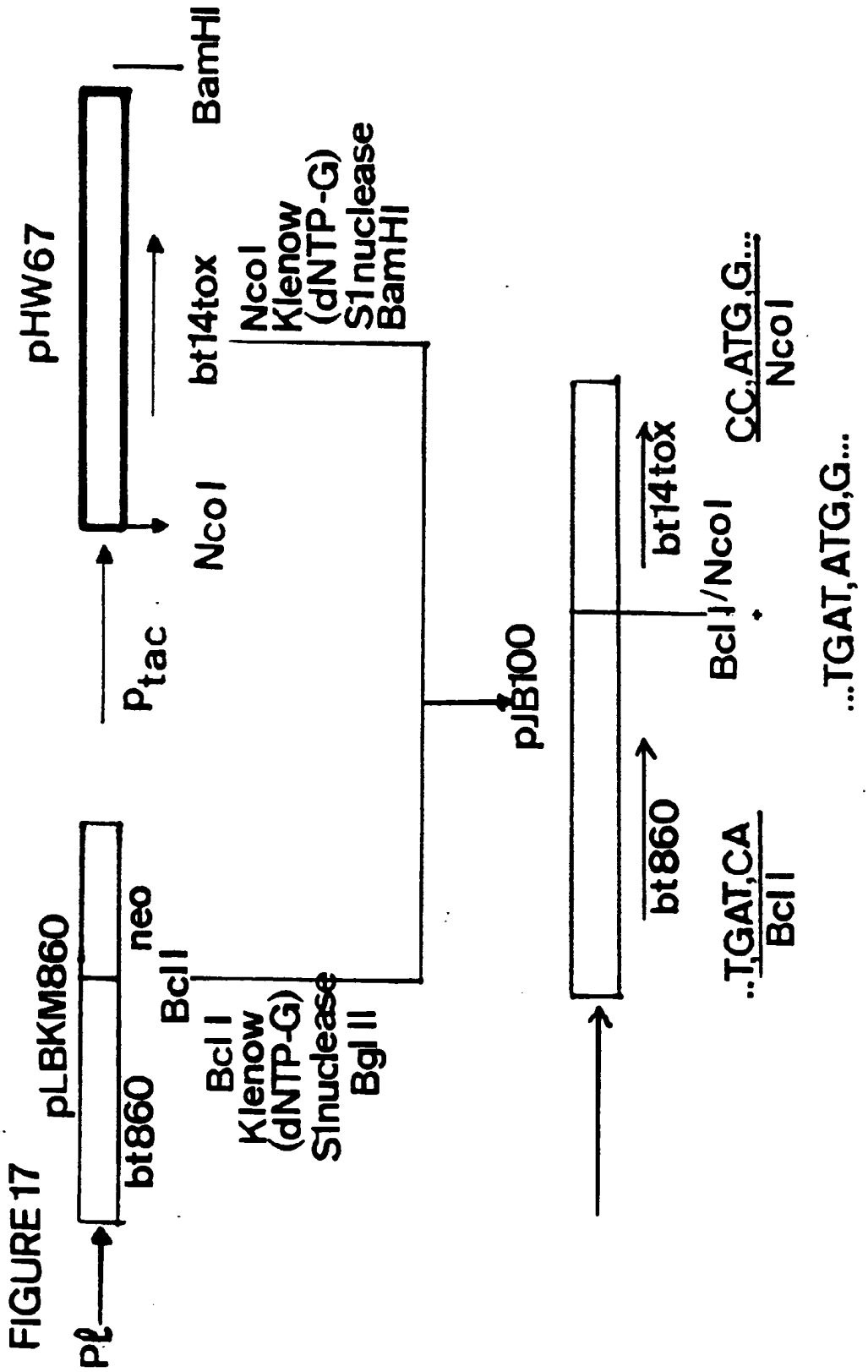


FIGURE 17
pLBKM860
neo
bt860
BclI
BclI
Klenow
(dNTP-G)
S1nuclease
BglII
pJB100
pHW67
BamHI
bt14tox
NcoI
Klenow
(dNTP-G)
S1nuclease
BamHI
NcoI
Ptac
bt860
bt14tox
BclI/NcoI
..TGAT,CA
BclI
CC,ATG,G...
NcoI
...TGAT,ATG,G...